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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March Run on:

6, 2006, 16:13:17; Search time 122 Seconds (without alignments) 208.189 Million cell updates/sec

US-09-809-060A-2 Title: Perfect score:

36 1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36 Sequence:

2166443 segs, 705528306 residués

Gapop 60.0 , Gapext 60.0

OFIGO

Scoring table:

Searched:

0

2166443 Total number of hits satisfying chosen parameters: Word size :

RESULT 1

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Databáse :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

SUMMARIES

	Description	Q6wh50 human immun	Q80161 human immun	P03378 human immun	Q7zjr9 human immun	Q9ea82 human immun	Q9ijn5 human immun	Q6v8z2 human immun	Q6v8y8 human immun	Q7zc84 human immun	Q7zce4 human immun	Q6ya57 human immun	P19549 human immun	092761 human immun	Q73303 human immun	Q9elr7 human immun	Q8q865 human immun	Q8q867 human immun	Q8q863 human immun		Q9e610 simian-huma	Q5d7p6 human immun	Q5d7g3 human immun	Q9eaaS human immun	Q9yxm9 human immun	Q9yxr6 human immun	OSucio human immun	Q7zc86 human immun	Q7zc94 human immun	Q7zcb0 human immun	Q7zcbl human immun	Q7zcb7 human immun
SUMMARIES	ID	Q6WH50_9HIV1	Q80161_9HIV1	ENV HVIA2	Q72JR9 9HIV1	Q9EA82_9HIV1	Q91JNS_9HIV1	Q6V8Z2_9HIV1	Q6V8Y8_9HIV1	Q7ZC84_9HIV1	Q7ZCE4_9HIV1	Q6YA57 9HIV1	ENV HV1S3	092761_9HIV1	Q73303_9HIV1	Q9E1R7_9HIV1	Q8Q865_9HIV1	Q8Q867_9HIV1	Q8Q863_9HIV1	Q9E1S7_9HIV1	Q9E610_9PLVG	Q5D7P6_9HIV1	Q5D7Q3_9HIV1	Q9EAA5_9HIV1	Q9YXM9 9HIV1	Q9YXR6 9HIV1	Q5UCI0_9HIV1	Q72C86_9HIV1	Q72C94_9HIV1	Q72CB0_9HIV1	Q7ZCB1_9HIV1	Q7ZCB7 9HIV1
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IV1 Q7zce3 human	-	-	-		1 Q7zc14	-	1 Q6bc08	1 Q72940	-	9HIV1 Q7zc13 human		IV1 Q6wh02 human	IV1 Q4vup4 human	ENTS
07ZCE3 9H	QBJAL6 9H	Q6JE16_9H	Q6EFV9_9H	Q7ZC12_9H	Q7ZC14_9H	Q6B4P1_9H	Q6BC08_9H	Q72940_9H	Q7ZC11_9H	Q7ZC13_9H	Q69910_9H	Q6WH02 9H	Q4VUP4_9H	ALIGNMENTS
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144	199	845	849	849	849	850	828	859	868	898	42	117	120	
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σ	53	29	29	53	53	53	53	53	53	53	27	27	27	
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PubMeda14715797; DOI=10.1128/JCM.42.1.426-430.2004; Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G., Gouvea M.I.F.S., Guimaraes M.A.A.M., De Oliveira F.B., Magnanini M.M.F., Brindeiro M., Tanuri A.; Esperanza C.B., "Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naive, infected individuals in the army health service of Rio de Janeiro, Brazil."; J. Clin. Mczebiol. 42:426-430(2004).
SMR: Q6WH50; 1-105.
                                                                                                                     Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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122 AA; 14775 MW; 66674BB2877E73FB CRC64;
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                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope glycoprotein (Fragment).
   122 AA
   PRT;
QEWHSO 9HIV1 PRELIMINARY;
QEWHSO;
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78 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 113 1 YTNTIYTLLEBSQNQQEKNEQELLELDKWASLWNWF 36

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Gaps

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Length 122; 0; Indels

100.0%; Score 36; DB 2; 100.0%; Pred. No. 2.9e-27; iive 0; Mismatches 0;

Query Match
Best Local Similarity 100.0
Matches 36, Conservative

Last sequence update) Last annotation update) 853 AA 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-JUN-2003 (TrEMBLrel. 24, Last anno
Bracolop polyprotein. PRT; QB0161 9HIV1 PRELIMINARY; Q80161; 9HIV1 RESULT 2 080161 1D 08 AC . 08 DT 01 DT 01 DE ET 03 HV

Human immunodeficiency virus 1.

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Transmembrane.
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Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                           Human immunodeficiency virus type 1 (isolate ARV2/SF2) (HIV-1).
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] — NUCLEOTIDE SEQUENCE (GENOMIC RNA).
NUCLEOTIDE SEQUENCE (GENOMIC RNA).
MEDLINE-85090453; PubMed=2578227;
Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
Stemplen M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
Stemplen M.M., Dina D., Luciw P.A.;
Levy J.A., Dina D., Luciw P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP12)].
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Pred. No. 1.6e-26;
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PIR; A03976; VCLJA2.
                         Lentivirus; Primate lentivirus group
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SMR; P03378; 199-490, 539-625.
KIV; K02007; ENVSSP2.
INTERPC; IPR000328; ENV GP41.
INTERPC; IPR000777; GP120.
PEam; PF00216; GP120; 1.
PEam; PF00517; GF41; 1.
AIDS; Capsid protein; Glycoprote
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                                              NCBI_TaxID=11676;
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ENV HV1A2

ID PENV HV1A2

AC P03378;
BT 21-JUL-1986

DT 21-JUL-1986

DT 21-JUL-1986

DT 31-SEP-2005

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RN MEDLINE=856

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MEDLINE=22800244; PubMed=12921095; DOI=10.1089/088922203322231003;
Swanson P.A., Devare S.G., Hackett J.R. Jr.;
"Molecular Characterization of 39 HIV-1 Isolates Representing Group M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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Transmembrane glycoprotein.
4-linked (GlcNAc. . .) (Pot
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Q7ZJR9_9HIV1 PRELIMINARY; PRT; 122 AA.
Q7ZJR9;
Q1_JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 1.6e-26;
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MEDLINE=20346416; PubMed=10890362; DOI=10.1089/08892220050058425; MASCIOLTA S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A., Baggs J., Lal R., Pieniazek D.; Talla B., Buloso W., Clara L., Tanuri A., Ramos A., Evidence for a high frequency of HIV-1 subtype F infections among heterosexual population in Buenos Aries, Argentina."; ALDS Res. Hum. Retroviruses 16:1007-1014(2000). EMBI, AF220697; AAF76816.1; -; Genomic_DNA.
                                                                                                                                      Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae, Lentivirus, Primate lentivirus group.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Akoozek A., Ozkan E., Calangu S., Altas K.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY347737; AAQ63672.1; -; Genomic_DNA.
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122 AA; 14779 MW; C9B2C8944C48C614 CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019089; F:structural molecule activity; IEA.
InterPro; FF00517; GP41.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
Q9IJNS;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope glycoprotein (Fragment).
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100.0%; Pred. No. 2.4e-23;
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88.9%; Score 32; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                      Human immunodeficiency virus 1.
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127 AA;
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Best Local Similarity
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EMBL, AF190970; AAG02332.1; -; Genomic_DNA.
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  (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
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14745 MW; 2244648573D7BFF9 CRC64;
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122 AA; 14804 MW; CF6AF2DC9EDA9C69 CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019189; F:erructural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
                                                                                                              GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; P:structural molecule activity; IEA.
InterPro: IPRO0517; GP41; 1.
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0. 2.3e-23;
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EMBL, AV214090; AA061810.1; -; Genomic_RNA.
HSSP; P04624; 1JAU.
SMR; Q7ZJR9; 1-105.
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Q91JNS 9HIV1
ID Q9IJNS_9HIV1 PRELIMINARY;
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Q9EA82;
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Best Local Similarity
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MEDLINE-22679027; PubMed=12794544;

MEDLINE-22679027; PubMed=12794544;

MEDLINE-22679027; PubMed=12794544;

Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.; "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HIV-1 strains."; The strains."; Genomic_RN3912003).

EMBL, AY185376; AAO65651.1; -; Genomic_RNA.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                        88.9%; Score 32; DB 2; Length 144; 100.0%; Pred. No. 2.7e-23;
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144 AA; 16863 MW; ADGC57B998454949 CRC64;
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144 AA; 16856 MW; 204A5328B6EE248C CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019198; Fstructural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
      GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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01-JJN-2003 (TrEMBLrel. 24, Created)
01-JJN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 2.7e-23;
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100.0%; Pred. No. ...
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Matches 32; Conservative 0; Mismatches
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                                                    InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
Envelope protein.
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SEQUENCE 144 AA; 16863 MW; A
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Name=env,
Human immunodeficiency virus 1.
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QGXAS7 9HIV1 PRELIMINARY;
QGYAS7;
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DOI=10.1097/00126334-200306010-00003;

Roman F., Gonzalez D., Lambert C., Derroo S., Fischer A., Baurith T., Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;

"Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-nalve patients infected with subtype B and non-B HIV-1 strains."; Genomic_RNA:

SAGUIT. Immune Defic. Syndr. 33:134-139(2003).

EMBL. AX18545, AA065711.1; -; Genomic_RNA.

SNR; QYZC84; 11-99.

GO: GO:0016021; C:integral to membrane; IEA.
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Lentivirus; Primate lentivirus group.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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141 AA; 16814 MW; B6A0F119928C26A1 CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019198; Fistructural molecule activity; IEA.
Intervo; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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Local Similarity 100.0%; Pred. No. 2.6e-23;
Hes 32; Conservative 0; Mismatches 0;
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QEVBYB;
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Q7ZC84;
32; Conservative
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NUCLEOTIDE SEQUENCE.
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protein; Glycoprotein; Polyprotein; Signal;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Exterior membrane glycoprotein.
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NULEOTIDE SEQUENCE.
MEDIINE=88178716; PubMed=9519894;
McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 852;
1.3e-22;
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Pfam; PP00516; GP120; 1.
Pfam; PP00517; GP41; 1.
D-structure; AIDS; Capsid protein Structural protein; Transmembrane. SIGNAL By si:
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092761;
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nes 32; Conservative
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852 AA;
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CARBOHYD
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
MUCLBOTIDE SEQUENCE [GENOMIC DNA].
MUCLINE=90317906; PubMed=2370688;
Vork-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
Whuman immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
NCBI_TaxID=11690;
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.
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                                                                                                                  MEDLINE=22866095; PubMed=14506784; DOI=10.1089/088922203322280937; Swanson P., Devare S.G., Hackett J.Dr.; Pull-length sequence analysis of HIV-1 isolate CM237: a CRF01_AE/B intersubtype recombinant from Thailand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                                                                                                                                                                                                                                                     STRAIN=CM237;
Swanson P.A., Devare S.G., Hackett J.R. Jr.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX167123; AAO40783.1; -; Genomic_RNA.
HSSP; P04578; 1K33.
SWR; Q6YA57; 1-130, 100-348, 140-480, 529-615.
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AA; 95647 MW; 7A6654344CFD02AB CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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Pred. No. 1.3e-22;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                AIDS Res. Hum. Retroviruses 19:707-712(2003)
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PDB; 1MEQ; NMR; A=484-506.
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HIV; M38427; ENV$SF33.
ILLCEPED: IPRO000328; ENV GP41.
ILLCEFED: IPRO00777; GP120.
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Pfam; PF00517; GP41; 1.
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NUCLEOTIDE SEQUENCE.
                                                                               NUCLEOTIDE SEQUENCE
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SEQUENCE 845 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                      MCBI_TaxID=11676;
                                                                                                    STRAIN=CM237
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P19549;
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DT 13-SE

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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Manatels K.s.

Manatels According to the rescue and analysis of functional HIV-1
env genes: evidence for recombination in the vicinity of the tat/rev
splice site.";

AIDS 10:39-46(1996).

BENBL: U36877; AAC55537.1; -; Genomic_DNA.

PIR; A53591; A53591.

HSSP: P04578; IDLB.

SWR; O73303; 81-125, 197-488, 536-622.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.
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NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
DOUGLAB N.W., Knight A.I., Hayhurst A., Barrett W.Y., Kevany M.J.,
Daniels R.S.;
Sheppard W.H.;

"Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in San Francisco Men's Health Study participants.";

ALDS Res. Hum. Retroviruses 14:329-337(1998).

EMBL; AF025750; AAC40588.1; -; Genomic_DNA.

EMSP; PO0871; 1GE4.

SNR; 092761; 535-622.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

InterPro; IPR000328; Env GP41.
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Pfam; PF00517; GP41; 1.
AIDS; Envelope protein; Transmembrane.
SEQUENCE 852 AA; 96544 MW; 3C7780DB0611E617 CRC64;
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Pfam; PF00517; GP41; 1.
AIDS; Envelope protein; Transmembrane.
SEQUENCE 852 AA; 96808 MW; A24BA64A133D149B CRC64;
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Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.9%; Score 32; DB 2; Li
100.0%; Pred. No. 1.3e-22;
:ive 0; Mismatches 0;
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InterPro; IPR000777; GP120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 01, (TrEMBLrel. 24,
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RESULT 15 Q9E1R7_9HIV1

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MUCLEOTIDE SEQUENCE.

MEDLINE=20442410; Pubmed=10984542; DOI=10.1073/pnas.97.19.10532;

MEDLINE=20442410; Pubmed=10984542; DOI=10.1073/pnas.97.19.10532;

MEDANAI C.B., John W., Garr J.K., Edwards J., Mahabir B., Sill A.,

McDanal C.B., Connolly S.M., Goodman D., Bennette R.Q., O'Baten T.R.,

Weinhold K.J., Bartholomew C., Blattner W.A., Greenberg M.L.;

"A distinctive clade B HIV type I is heterosexually transmitted in

Proc. Natl. Acad. Sci. U.S.A. 97:10532-10537(2000).

FMEL AR277(71; AAG22514.1; -; Genomic_DNA.

SMR, Q9E1R7; 539-625.
                                                                                                                                                                                                      Human immunodeficiency virus 1.
Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
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Pred. No. 1.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIDS; Envelope protein; Transmembrane.
SEQUENCE 855 AA; 97102 MW; 26271D6CCCCCFFAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0000199; Figuratural molecule activity; IEA.
InterPro; IPR000378; ENV GP41.
InterPro; IPR000777; GP120.
                                                      01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641 IYTLLEESONOOEKNEOELLELDKWASLWNWF 672
         855 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ... 0; Mismatches
      PRT;
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Q9E1R7_9HIV1 PRELIMINARY;
Q9E1R7;
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Pfam; PF00517; GP41; 1.
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nes 32; Conservative
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11676;
                                                                                                                                                     Envelope protein.
                                                                                     01-MAR-2001
01-JUN-2003
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Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1051, Ap Sequence 1051, Ap

Sequence Seq

Perfect score:

Run on:

Sequence:

Scoring table:

Word size :

Searched:

Database :

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APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Sham O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 36;
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CONFUTER:

COMPUTER READABLE FORM:

MEDIUM TYPE:

COMPUTER:

                                                                                                                                                    US-09-082-279B-856
US-09-315-304B-856
US-09-513-965A-856
US-09-350-641C-856
US-09-350-641C-856
US-09-350-641B-856
US-08-965-056-28
US-08-965-056-28
US-08-961-078-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-082-279B-1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08486099
Patent No. 6013263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acide
TYPE: amino acid
STRANDEDNESS:
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; MOLECULE TYPE: peptide
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TELEX: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-486-099-3
Query Match
Sequence 1357, Ap
Sequence 1357, Ap
Sequence 1357, Ap
Sequence 1357, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
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3, Appli
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                                                                                                                                                                                                              March 6, 2006, 16:25:38 ; Search time 28.6667 Seconds (without alignments) 103.825 Million cell updates/sec
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Sequence
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                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PGTUS COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                  YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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S-09-834-784-1357
S-09-51S-965A-1357
S-09-350-641C-1357
S-09-350-841A-1357
S-09-487-26A-3
S-09-623-548A-1421
S-10-252-136-3
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| S-08-474-349A-3
| S-09-315-304B-1357
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S-08-485-551A-3
S-08-471-913A-3
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                                                                                                                                                    OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
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STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-475-668A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-919-597-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                              APPLICANT: Belognest, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lamplois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
THILE OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
                           ö
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100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: O7-UNN-1995
CLASSIFICATION: 435
                                                                                             1 YINTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
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                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Pennie & Edmonds LLP
T: 1155 Avenue of the Americas
New York
: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
                                                                                                                                                                                                                   Sequence 3, Application US/08484223B Patent No. 6020459 GENERAL INFORMATION:
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-484-2238-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-08-919-597-3
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Sequence 3, Application US/08919597 Patent No. 6054265 GENERAL INFORMATION: APPLICANT: Bolognes, Dani P. APPLICANT: Matthews, Thomas J.

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APPLICANT: Lambett, Dennis M.
APPLICANT: Lambiolos Alphones J.
APPLICANT: Lambiolos Alphones J.
APPLICANT: Den Company M.
APPLICANT: Lambiolos Alphones J.
APPLICANT: Den Company M.
APPLICANT: Den Company M.
APPLICANT: Lambiolos Alphones J.
APPLICANT: Lambiolos Alphones J.
APPLICANT: Lambiolos Alphones J.
APPLICANT: Lambiolos Alphones J.
APPLICANT: New York
COMPANY: New York
C
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Gaps

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GENERAL INFORMATION:
APPLICANT: Balognest, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois Alphones J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TUSION-ASSCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                Length 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CARRENT APPLICATION DATH:
APPLICATION UNMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                            1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                         ; Score 36; DB 2;
; Pred. No. 2.8e-27;
0; Mismatches 0;
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100.0%; Score 36; DB
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Pennie & Edmonds LLP
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08471913A Patent No. 6093794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
  (212) 869-9741/8864
                                                                                                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 790-9090
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 36; Conservative
                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                     TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Ne COUNTRY:
    TELEFAX:
TELEX: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-471-913A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels . 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 36; DB 2; Length 36; 100.0%; Pred. No. 2.8e-27; Live 0; Mismatches 0; Indels
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
HTLING BATE: 07-JUN-1995
FTLING BATE: 07-JUN-1995
FTLING BATE: 07-MATION:
                                                                            CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,66BA

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTONEY/AGENT INPORMATION:

NAME: CCTULZZ, LAURE 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEFAX: (212) 790-9090

TELEFAX: (212) 790-9090

TELEFAX: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YINTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08485551A
Patent No. 6068973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Sham O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR TITLE OF INVENTION: TRANSMISSION TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petteway, Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolognesi, Dani P.
Matthews, Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 36 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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LENGTH: 36 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-474-349A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Stephen R.
APPLICANT: Lambort, Stephen R.
APPLICANT: Lambort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA

ZIP: 10036-2711

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: O'-JUN-1995
CLASSIFICATION: 435
ATTOMNEY/AGENT INPORMATION:
NAME: CCCLUZZ, LAULE A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
TELER: 66141 PERNIE
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                    YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YTNTIYTLLEESQNQQEKNEGELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1357, Application US/09082279B
Patent No. 6258782
                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08485264A Patent No. 6228983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 amino acids
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Guthrie, Kelly
Merutka, Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Barney, S
APPLICANT: Guthriae,
APPLICANT: Merutka,
APPLICANT: Anwer, Mo
APPLICANT: Lambert,
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bologn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-082-279B-1357
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Anyer, Mohmed Lambert, Dennis

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APPLICANT: Bolognesi, Dani P.
APPLICANT: Matchews, Thomas J.
APPLICANT: Matchews, Thomas J.
APPLICANT: Matchews, Thomas J.
APPLICANT: Matchews, Thomas J.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES FILE STREAMER: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILLING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1357
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELERRAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 36; DB 2; ]
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08474349A Patent No. 6333395
                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Seguence
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
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ORGANISM: Human immunodeficiency virus
                                                                                                 7872-010
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                                 ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 7872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08470896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                    (212) 790-9090
(212) 869-9741/8864
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Best Local Similarity 100.0
Matches 36; Conservative
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                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               36 amino acids
                                                                                                                                                                                                                                                              TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-255-208A-3
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                    amino acid
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Matches 36; Conserv
                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                             LENGTH:
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APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT PILION DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
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...reliCANT: Barney, Shawn O.
. APPLICANT: Lambert, Dennis M.
. TITLE OF INVENTION: TSYNTHETIC PEPTIDE INHIBITORS OF HIV TITLE OF SEQUENCES: 111
. CORRESPONDENCE ADDRESS:
...STRPF".
STRPF".
STRPF".
STRPF".
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                                      Indels
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                     2.8e-27;
                                                                                                              1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                                           1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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 100.0%; Score 36; DB 2; 100.0%; Pred. No. 2.8e-27
                                      0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/255,208A
                                                                                                                                                                                                        Sequence 1357, Application US/09315304B Patent No. 6346558 GENERAL INFORMATION: APPLICANT: Barney, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Core polypeptide US-09-315-304B-1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08255208A Patent No. 6440656 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 36; Conservative
                                      36; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                 Guthrie, K.
Merutka, G.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: USA
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US-09-315-304B-1357
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US-08-255-208A-3
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APPLICANT:
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APPLICANT: Johnson, M. Ross
APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIC
TITLE OF INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: 10/80/973,952A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
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Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
VENTION: TRANSMISSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 36; DB 2; I Similarity 100.0%; Pred. No. 2.8e-27; 36; Conservative 0; Mismatches 0;
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Score 36; DB 2;
Pred. No. 2.8e-27;
                                                        0; Mismatches
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6, 2006, 16:27:50
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Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Core polypeptide
                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTRA A, 742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELECOMUNICATION INFORMATION:
TELEFRONE: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
    07-JUN-1995
                                                                                                                                                                                                                                                                        36 amino acids
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March
Job time: 28.6667 secs
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US-09-834-784-1357
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FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TRANSMISSION
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100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                           CUDNIKY: 0.25A

CUNTRY: 0.25A

CUNTRY: 0.25A

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPTTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: COLUZZ, LAURA A.

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION INFORMATION:
TELEFPHONE: (212) 790-9090

TELEFPHONE: (212) 869-9741/8864

TELEFPKX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLACATION DATA:
APPLICATION NUMBER: US/08/485,546A
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                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: FUSION-ASSOCITITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPER: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3, Application US/08485546A; Patent No. 6518013; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-896-3
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
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: USA
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                                                                                     New York
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                                                                                                                                    USA
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TELEX: 60
                                                                                                                                 COUNTRY:
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US-08-485-546A-3
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  Score 36; DB 2; Length 36; Pred. No. 2.8e-27;
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                                                 Indels
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APPLICANT: Gally,
APPLICANT: Merutka, Gene
APPLICANT: Anwer. Mehned
APPLICANT: Anwer. Mehned
APPLICANT: Anwer. Mehned
APPLICANT: Anwer. Mehned
TITLE OF INVENTION: PHARMACKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 109/082,279
FRIOR APPLICATION NUMBER: 09/082,279
FRIOR APPLICATION NUMBER: 09/082,279
FRIOR APPLICATION NUMBER: 1938-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE FRAISEQ for Windows Version 3.0
SEQ ID NO 1357
LENGTH: 36
                                                                                                                                Query Match
100.0%; Score 36; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                   1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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Query Match
100.0%; Score 36; DE
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 36; Conservative 0; Mismatches
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:

6, 2006, 16:19:28; Search time 19 Seconds (without alignments) 182.305 Million cell updates/sec March

US-09-809-060A-2

Title: Perfect score:

1 YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36 Sequence:

Gapop 60.0 , Gapext 60.0 OLIGO Scoring table:

283416 segs, 96216763 residues Searched:

Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR_B0:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de	•		SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	36	100.0	855	i -	VCLJA2	env polyprotein pr
7	27	75.0	357	~	S21994	lope protein
m	27	75.0	357	~	S21996	
4	27	75.0	443	N	C41621	env polyprotein P
S	27	75.0	847	N	T09448	envelope glycoprot
9	27	75.0	847	~	S13289	env protein - huma
7	27	75.0	851	N	S33985	env polyprotein -
80	27	75.0	854	~	S13288	env protein - huma
σ	27	75.0	856	Н	VCLJ3W	env polyprotein pr
10	27	75.0	856	Н	VCLJH3	
11	27	75.0	861	Н	VCLJSC	
12	27	75.0	861	٦	VCLJLV	protein
13	25	69.4	358	N	821998	protein
14	22	61.1	357	N	S21992	envelope protein g
15	22	61.1	853	~	S54384 .	envelope polyprote
16	22	61.1	855	٦	VCLJZR	env polyprotein pr
17	. 55	61.1	859	ч	VCLJMN	
18	21	58.3	856	Н	VCLJVL	env polyprotein pr
19	16	44.4	852	~	T12016	envelope glycoprot
20	15	41.7	357	N	S22004	envelope protein g
21	15	41.7	357	~	S22006	envelope protein
22	15	41.7	846	Н	VCLJND	env polyprotein pr
23	15	41.7	852	-	VCLJBR	
24	15	41.7	859	~	T01672	envelope polyprote
25	13	36.1	357	~	S21990	envelope protein g
56	13	36.1	843	-	H44001	env polyprotein pr
27	12	33.3	358	~	S70417	envelope protein g
28	12	33.3	358	α.	822000	
29	12	33.3	358	N	S22002	envelope protein g

env polyprotein M	env polyprotein D	env polyprotein pr	env polyprotein pr	env polyprotein -	catechol oxidase (catechol oxidase (catechol oxidase (env polyprotein pr	envelope polyprote	envelope polyprote	cysteine synthase	hypothetical prote	glutamate dehydrog	catechol oxidase (catechol oxidase (
A41621	B41621	VCLJKX	VCLJKB	VCLJH4	T03682	S33540	T07097	VCLJSI	JU0266	JT0954	C90179	T19415	G69933	S34785	830930
~	~	-	н	٦	N	-	~	-	N	~	~	N	~	~	N
445	454	729	861	898	592	596	599	854	136	136	297	425	426	583	583
33.3	33.3	33.3	33.3	27.8	22.2	22.2	22.2	22.2	19.4	19.4	19.4	19.4	19.4	19.4	19.4
12	12	12	12	70	80	80	80	80	7	7	7	7	7	7	7
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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ES	
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- human immunodeficiency virus type 1 (isolate ARV-2) N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004

Risanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi Science 227, 484-492, 1985 Affitle: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2). A;Reference number: A04003; MUID:85090453; PMID:2278227

A; Molecule type: DNA Accession: A03976

A,Residues: 1-855 <SAN> A,Cross-references: UNIPROT:P03378; UNIPARC:UP1000012A00F; GB:K02007; NID:g328658; PIDN:

A/Gene: env C;Superfamily: type E retrovirus env polyprotein C;Superfamily: type E retrovirus env polyprotein; dimunodeficiency; polyprote C;Reywords: AlDS; capsid protein; coat protein; dlycoprotein; immunodeficiency; polyprote F;31-509/Product: exterior membrane glycoprotein #status predicted <EXT> F;510-855/Product: transmembrane glycoprotein #status predicted <TWM> F;510-855/Product: transmembrane glycoprotein #status predicted <TWM> F;87,129,140,158,184,190,200,244,265,298,304,334,341,358,364,388,394,400,408,445,458, F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted DB 1; 1 8.3e-28; Query Match
100.0%; Score 36; DE
Best Local Similarity 100.0%; Pred. No. 8.3
Matches 36; Conservative 0; Mismatches

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Gapa

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0; Indels

637 YINTIYILEESQNQQERNEQELLELDKWASLWNWF 672 1 YTNTIYTLLEESONQOEKNEQELLELDKWASLWNWF 36 ઠે g

RESULT 2

envelope protein gp120/gp41 - human immunodeficiency virus type 1 C;Species: human immunodeficiency virus type 1, HIV-1

A,Variety: isolate 27B C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: \$21994; \$70421 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W. submitted to the EMBL Data Library, July 1991 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determir

A;Accession: S21994
A;Molecule type: DNA
A;Residues: 1-357 <STE1>
A;Cross-references: UNIPROT:Q78118; UNIPARC:UP10000178606; EMBL:X61355; NID:g60179; PIDN:
A;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

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Query Match
Best Local Similarity 100.
Matches 27; Conservative
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A;Molecule type: DNA
A;Residues: 1-847 <OBR>
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Best Local Si
Matches 27,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 870422, 821996
C;Accession: 870422, 821996
A;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 33-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebra A;Reference number: 870417; MUID:92144209; PMID:1736940
A;Reference number: S70417; MUID:92144209; PMID:1736940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Molecule type: DNA
A;Residues: 1-357 <ST2>
A;Residues: 1-357 <ST2>
A;Cross-rose: UNIPROT: Q78119; UNIPARC: UPI0000104EC6; EMBL: X61356; NID: g60181; PIDN
A;Experimental source: patient 27L
A;Note: submitted to the EMBL Data Library, July 1991
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: type E retrovirus env polyprotein
C; Superfamily: type E retrovirus env polyprotein; glycoprotein; immunodeficiency; polyprot
F;1-251, Product: coat protein gp120 (fragment) #Bratus predicted <GP1>
F;252-443/Product: coat protein gp41 (fragment) #Bratus predicted <GP2>
F;424-443/Domain: transmembrane #Bratus predicted <TMN>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,355,377/Binding site: ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Peb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: C41621
R;Burger, H; Weiser, B; Flaherty, K; Gulla, J; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 1123-11240, 1991
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: C41621
A, Molecule type: DNA
A, Residues: 1-443 < BURA
A, Cross-treferences: UNIPROT: Q80023; UNIPARC: UPI0000104256; GB: M77230; NID: g328631; PIDN
A, Note: this virus was isolated from the mother's sexual partner
C, Genetics:
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A;Cross-references: UNIPARC:UPI00000FF05F; EMBL:X61355; NID:g60179
C;Superfamily: type E retrovirus env polyprotein
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                                                                                                                                                                                                                                                                                                              y Match 75.0%; Score 27; DB 2; Length 357;
Local Similarity 100.0%; Pred. No. 2.8e-19;
hes 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 27; DB 2; Length 357, 100.0%; Pred. No. 2.8e-19;
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Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 EESQNQQEKNEQELLELDKWASLWNWF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EESQNQQEKNEQELLELDKWASLWNWF 174
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                                                                                                                                   preliminary
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A; Status: preliminary
                                                                                                                                                                 A; Molecule type: DNA
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13289
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A;Tille: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gpl20 c
A;Reference number: S13288; MUID:91043044; PMID:2172833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q75760; UNIPARC:UP1000010C516; EMBL:U63632; NID:g1465777; PII
                                                                                                                                                                                                                                                                                                                                                 C;Accession: T09448
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitter to the EMBL Data Library, July 1996
A;Reference number: 216673
A;Accession: T09448
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Receule type: DNA
A;Residues: 1-847 <PAN>
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                                                                  Gaps
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C;Superfamily: type E retrovirus env polyprotein
                 Score 27; DB 2; L Pred. No. 3.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 6.4e-19;
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100.0%; Pred. No. 6.4e-1!
trive 0; Mismatches
75.0%; Sco...
100.0%; Pred. No...
0; Mismatches
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                                                                                                                                         387 EESQNQQEKNEQELLELDKWASLWNWF 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FESONOGEKNEGELLELDKWASLWNWF 664
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BH10)

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R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F. A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; MUID:85111123; PMID:2578615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: type E retrovirus env polyprotein
C; Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;31-556/Product: transmembrane glycoprotein #status predicted <TMM>
F;812-856/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
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R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Stae
Virology 164, 531-536, 198
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
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A,Molecule type: DNA
A,Residues: 1-861 <GUR>
A,Residues: 1-861 <GUR>
A,Forestion: Serion of the serion of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-856 <RAT>
A;Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K0200
                                                              - human immunodeficiency virus type 1 (isolate HTLV-III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC) NiAlternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Home sapiens (man) C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
                                                                                                                       NiAlternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May, 1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.0%; Score 27; DB 1; Length 856; Best Local Similarity 100.0%; Pred. No. 6.4e-19; Matches 27; Conservative 0; Mismatches 0; Indels
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Matches 27; Conservative
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C;Superfamily:
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                                             A;Residues: 1-851 <CAR>
A;Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:g60192; PIDN
C;Superfamily: type E retrovirus env polyprotein
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A;Residues: 1-856 <STA>
A;Cross-references: UNIPROT:P31872; UNIPARC:UPI000012A024; GB:K03455; GB:M38432; NID:919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C;Accession: S13288
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
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R;Starcich, B.K.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, Call 45, 637-648, 1986
A;Title: Identification and characterization of conserved and variable regions in the A;Reference number: A24774; MUID:86218077; PMID:2423250
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Species: human immunodeficiency virus type 1, HIV-1
pate: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
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Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 27; Conservative 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-854 <OBR>
A;Cross-references: UNI)
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A; Molecule type: mRNA
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- human immunodeficiency virus type 1 (isolate LAV-1a) C; Species: human immunodeficiency virus type 1, HIV-1 env polyprotein precursor N; Alternate names: coat po

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                                                                            A;Accession: S70424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <ST2>
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Job time : 20 secs
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C; Superfamily: type E retrovirus env polyprotein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>F;1-30/Opmain: signal sequence #status predicted <SIG>F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>F;31-516/Product: transmembrane glycoprotein #status predicted <TWM>F;817-561/Product: transmembrane glycoprotein #status predicted <TWM>F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
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S21998
Circle protein gpl20/gp41 - human immunodeficiency virus type 1
Cispecies: human immunodeficiency virus type 1
Cispecies: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 28
Cispecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
Cispeciesion: S21998; S70425
Ristenler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Ristenler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A;Bestription: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determine A;Reference number: S21990
A;Accession: S21998
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A Molecule type: DNA
A Molecule type: DNA
A Molecule type: 1-38 of STEL-
A Molecule type: UNIPROT: Q78120; UNIPARC: UPI0000178607; EMBL: X61359; NID: g60182; PIDN
R Moleculer, H.; Storch-Hagenlocher, B.; Wildemann, B.
A Mole Res. Hum. Retrovituses 8, 35-59; 1992
A Moleculer type: The Moleculer type 1 in blood and cerebt A Molecule to Daylations of human immunodeficiency virus type 1 in blood and cerebt A Molecule number: S70417; MUID: 92144209; PMID: 1736940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reaidues: 1-222,'X', 224-358 <STE2>
A;Cross-references: UNIPARC:UP100000FE72C; EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-861 <WAI>
A;Cross-references: UNIPROT:P03377; UNIPARC:UPI000012A013; GB:K02013; NID:G326417; PIDN:
C;Genetics:
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                                         17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
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A; Note: host Homo sapiens (man)
C; Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change
C; Accession: A03975
R; Wain-Hobson, S; Sonigo, P; Danos, O;; Cole, S;; Alizon, M.
Cell 40, 9-17, 1985
A; Title: Nucleotide sequence of the AIDS virus, LAV.
A; Reference number: A90866; WUID:85099333; PMID:2981635
A; Accession: A03975
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A,Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro A,Reference number: S70417; MUID:92144209; PMID:1736940
                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q78112; UNIPARC:UP10000107A48; EMBL:X61358; NID:g60177; PIDN: A;Exporimental source: patient 2.2
A;Exporimental source: patient 2.2
A;Note: submitted to the EMBL Data Library, July 1991
C;Superfamily: type E retrovirus env polyprotein
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150 SQNQQEKNEQELLELDKWASLW 171

A;Status: preliminary
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Residues: 1-853 «THE>
A;Cross-references: UNIPROT:P12487; UNIPARC:UP1000012A027; EMBL:M22639; NID:g329377; PIDN
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: polyprotein envelope polyprotein - human immunodeficiency virus type 1 C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004 submitted to the EMBL Data Library, July 1989 A, Reference number: \$54377 C, Accession: S54384 R, Theodore, T., Buckler-White,

Gaps 61.1%; Score 22; DB 2; Length 853; 100.0%; Pred. No. 5.5e-14;

ö 0; Indels 100.0%; Prec. ...

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completed: March 6, 2006, 16:26:19

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March Run on:

6, 2006, 16:26:33 ; Search time 97.3333 Seconds (without alignments) 154.540 Million cell updates/sec

US-09-809-060A-2 36 Title: Perfect score:

1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36 Sequence:

Scoring table:

1867569 segs, 417829326 residues Searched:

OLIGO Gapop 60.0 , Gapext 60.0

Total number of hits satisfying chosen parameters: 0 Word size :

1867569

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Appli	Appli	357, Ap	Appli	Appli	Appl	Appl	Appli	. Appli	1, Ap	Appl	Appl	Appl	Appl	App ,	Appl	Appl	Appl	1, Ap	App,	Appl	Appl	App	Appl	Appl	App,	, App
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IES		-060	-13	-64	-68	-748	-589	-28	-29	950-010-3	-697	-55	-321	-81	-81	-64	-10	-81	-10	-64	-01	-30	-30	-01	-30	-30	-0	-64
SUMMARIES		-809	-252-136	-351-641	-267-682	-267-7	-699-	-671-282	-168-295	-950	-990-	-131-551	10-000-	09-854-816-3	09-854-816	0-351-641-8	-018-102-	09-854-816	-018-102-1	0-351-641-1	-950	0-005-305-5	0-005-305	-950-010-	-005-305	0-005-305-7	-950-010-1	10-351-641
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Seguence 60, Appl	-	Sequence 200, App	Sequence 123, App	Sequence 794, App	61,	Sequence 70, Appl	Sequence 122, App	Sequence 86, Appl	641,		69		121,	802,	Sequence 63, Appl	Sequence 68, Appl	ò	
US-10-005-305-60	US-10-005-305-71	US-10-005-305-200	US-10-950-010-123	10-351-	US-10-005-305-61	US-10-005-305-70	US-10-950-010-122	08-09-608-60-SD	US-10-351-641-641	US-10-005-305-62	US-10-005-305-69	US-10-005-305-199	US-10-950-010-121	US-10-351-641-802	US-10-005-305-63	US-10-005-305-68	US-10-950-010-120	
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28	29	30	31	32	33	34	35	36	37 .	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Sequence 2, Application US/09809060; Publication No. US2020010317A1; GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
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100.0%; Score 36; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-2
                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF
SOFTWARE:
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1 YINTIYTLESSQNQQEKNEQELLELDKWASLWNWF 36 g

; Sequence 3, Application US/10252136; Publication No. US20030103998A1; GENERAL INFORMATION: US-10-252-136-3

APPLICANT: Johnson, M. Ross
APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNOBEFICIENCY VIRUS AND OTHER
TITLE OF INVENTION: VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORY THERAPY
TITLE OF INVENTION: USING COMBINATORY THERAPY
TITLE OF INVENTION: USING COMBINATORY THERAPY
CURRENT APPLICATION NUMBER: US/10/252,136
CURRENT FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: US/08/973,952
PRIOR PILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 3

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COUNTRY: USA
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Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT FILING DATE: 2003-01-24
CURRENT FILING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1999-05-20
PRIOR PLING DATE: 1999-05-20
PRIOR PLING DATE: 1998-05-20
PRIOR PLING DATE: 1998-05-20
PRIOR PLING DATE: 1998-05-20
SPIOR PRIOR PLING DATE: 1998-05-20
SPIOR PLING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 9.16-27;
Matches 36; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 9.1e-27;
tive 0; Mismatches 0;
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ADDRESSEE: Vennie & Edmonds
STREET: 1155 Avenue of the Americas
                        TYPE: PRT
ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1357, Application US/10351641 Publication No. US20030186874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Core polypeptide US-10-351-641-1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
APPLICANT: BOLOGNESI, Dani P. Matthews, Thomas J. Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 36; Conservative
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LENGTH: 36
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MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
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                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 36; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YINTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-0ct-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-UIN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bolognesi, Dani P. Matthews, Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wild, Carl T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
ULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
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Gapa
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TITLE OF INVENTION: Combination Method For Treating Viral Infections
FILE REFERENCE: INO1358

CURRENT APPLICATION NUMBER: US/10/168,295

CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: PCT/US01/48802

PRIOR APPLICATION NUMBER: 00/156,657

PRIOR APPLICATION NUMBER: 00/156,657

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BRIDON, Dominique P.
APPLICANT: BRIDON, Dominique P.
APPLICANT: DUFRESINE, Robert S.
APPLICANT: BOUDJELLAB, Missab
APPLICANT: ROBITAILLE, Martin
APPLICANT: MILMER, Peter G.
TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
TITLE OF INVENTION: INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                   Length 36;
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                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 4; Pred. No. 9.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YTNTIYTLLEESQNQQEKNEGELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 5;
Pred. No. 9.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Scoll 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 36; DB
Best Local Similarity 100.0%; Pred. No. 9.1
Matches 36; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/671,282
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,439
PRIOR FILING DATE: 2002-09-27,
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin version 3.2
SEQ ID NO 38
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 500862001501/REDC-1512
CURRENT APPLICATION NUMBER: US/10/950,010
CURRENT FILING DATE: 2004-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/US00/13651
PRIOR FILING DATE: 2000-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/623,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10168295 Publication No. US20050065319A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10950010 Publication No. US20050070475A1
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                                                                                                                                                                                                                                           FEATURE:
, OTHER INFORMATION: synthesized
US-10-671-282-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-10-168-295-3
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TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
TITLE OF INVENTION: their use in therapy
FILE REFERENCE: TRM-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
TITLE OF INVENTION: 9941-derived peptides, and its use in therapy
FILE REPERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 36; DB 4; I
100.0%; Pred. No. 9.1e-27;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative
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                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-267-748-3
                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                 FELEPHONE: (212) 790-9090
                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 38, Application US/10663589; Publication No. US20040063637A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Application US/10671282
Publication No. US20040122214A1
GENERAL INFORMATION:
  FILING DATE: 08-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthesized
                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38
LENGTH: 36
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                               FOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-10-663-589-38
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APPLICANT: GIRMLY, MILES APPLICANT: GIRMLY, MILES OF INVENTION: Peptides derived from a retrovirus of TITLE OF INVENTION: Peptides derived from a retrovirus of TITLE OF INVENTION: the HIV group, and their use NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner.
STREET: 3000 K Street, N.W., Suite 500
STREET: 3000 K Street, N.W., Suite 500
STREET: 0.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PAPELICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REGISTRATION NUMBER: 58315/106/BEAK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202,672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIPFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/394,021
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Sequence 1421, Application US/11066697

Publication No. U520050187159A1

GENERAL INPORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Bridon, Dominique P.
APPLICANT: Milner, Peter G.
APPLICANT: Milner, Peter G.
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PEPTIDAES ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: PEPTIDAES ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION NUMBER: 09/657,276
PRIOR PELICATION NUMBER: 60/153,406
PRIOR PELING DATE: 1999-09-10
PRIOR PERIOR DATE: 1999-09-10
PRIOR DATE: 1999-09-10
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                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide
US-11-066-697-1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: US 60/153,406
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 545
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 36
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Conservative
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Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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US-11-066-697-1421
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                                                                                                                       Length 145;
                                                                                                                                                              0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                         GUERTLER, Lutz
GUERTLER, Peptides derived from a retro
                                                                                                                                                                                                                            106 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                     Score 36; DB 3;
Pred. No. 3e-26;
                                                                                                                     Query Match
100.0%; Score 36; DB
Best Local Similarity 100.0%; Pred. No. 3e-
Matches 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/10000321
Publication No. US20020123039A1
GENERAL INFORMATION:
APPLICANT: BRUST, Stefan
KNAPP, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                             TOPOLOGY:
                                                                                US-09-131-551-11
                                                                                                                                                                                                                                                                                                                       US-10-000-321-11
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Sequence II, Application US/09131551; Publication No. US20010009667A1; GENERAL INFORMATION: APPLICANT: SRUST, Stefan APPLICANT: KNAPP, Stefan

RESULT 11 US-09-131-551-11

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CORRESPONDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Prancisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Making Same
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Andrew C. Braisted
J. Kevin Judice
                       SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              James A. Wells
    INFORMATION FOR SEQ ID NO: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS
                                                                   TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                              US-09-854-816-30
                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
JS-09-854-816-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Constrained Helical Peptides and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 36; DB 4; Length 145; 100.0%; Pred. No. 3e-26; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 YTNTIYTLLEBSONQOEKNEQELLELDKWASLWNWF 141
                                                                                PRIOR APPLICATION DATA:
PAPLICATION UNBER: 09/131,551
APPLICATION NUMBER: 09/131,551
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31.298
REFERENCE/DOCKET NUMBER: 58315/106/BEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: «UDKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Starovasnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Making Same
                                       FILING DATE: 04-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andrew C. Braisted
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melissa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCES:
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US-09-854-816-30
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                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Constrained Helical Peptides and Methods of
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                                                                                               Length 269;
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                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genettech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION SURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
                                                                                                                                                                                                                       169 YINTIYTLEESQNQQEKNEQELLELDKWASLWNWF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 204
                                                                                          Query Match
100.0%; Score 36; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.2e-26;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 36; DB 3; 1
100.0%; Pred. No. 5.2e-26;
tive 0; Mismatches 0;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
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RESULT 15
US-10-351-64-856
1 Sequence 865, Application US/10351641
2 Sequence 865, Application US/10351641
3 Genteral Information No. US20030186874A1
3 Genteral Information:
3 APPLICANT: Barney, S.
4 APPLICANT: Guthrie, K.
5 APPLICANT: Anwer, M.
5 APPLICANT: Anwer, M.
6 APPLICANT: Anwer, M.
7 TITLE OF INVENTION: PROPERTIES
8 TITLE OF INVENTION UNMER: 09/350,641
8 PRIOR FILING DATE: 1999-05-20
8 PRIOR FILIN
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Search completed: March 6, 2006, 16:32:48 Job time : 97.3333 secs

S IYTLLEESQNQQEKNEQELLELDKWASLWNWF 36

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1, Appli 7, Appli 8, Appli 9, Appli 2, Appli

Sequence Sequence Sequence

13381, A 6, Appli

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

App1

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Perfect score:

е ::

Run

Sequence:

Scoring table:

Word size :

Searched:

Minimum DB Maximum DB

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APPLICANI: BNN2., ...
RNAPP, Stefan
GERKEN, Manfred
GUERTLER, Lutz
TITLE OF INVENTION: Peptides derived from a retrovirus of
the HIV group, and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
CITY: Washington
CITY: Washington
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 58315/106/BEAK
                                                                                                                                                                                                                                                                                                               US-11-045-024-13381
US-11-112-277-6
                                                                                                                                                                          US-10-841-956A-19
US-11-151-598-1
US-11-151-598-7
US-11-151-598-8
                                                                                                                                                                                                                                                                                                                                                                                 US-11-112-277-36
US-11-112-277-38
US-11-151-598-10
                                                                 -10-506-796A-1
                                                                                        JS-10-506-796A-3
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US-11-151-598-2
                                                                                                                                                       US-11-151-598-4
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/11084858
Publication No. US20050271678A1
GENERAL INFORMATION:
APPLICANT: BRUST, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 145 amino acids
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
US-11-084-858-11
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                                                                                                                                                6, 2006, 16:28:08; Search time 10.3333 Seconds (without alignments) 69.679 Million cell updates/sec
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Sequence 35,
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Sequence
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Sequence
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Sequence
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7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-841-956A-1
US-11-102-03-1
US-11-187-687-23
US-11-112-277-33
US-11-187-647-24
US-10-841-956A-8
US-10-841-956A-8
US-10-841-956A-9
US-10-841-956A-9
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US-10-841-956A-9
US-11-053-100-27
US-11-053-100-30
US-11-053-100-33
US-11-053-100-33
US-11-053-100-33
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                                                                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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seq length: 200000000
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Match
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Result

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JS-11-187-687-22
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; Bublication No. US20050260194A1
; GENERAL INFORMATION:
    APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: STATTEL, JAMS TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: 60/487,904
; FRIOR FILING DATE: 2005-01-05
; FRIOR APPLICATION NUMBER: 60/487,964
; PRIOR PILING DATE: 2003-07-17
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 1
; LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                   | GENERAL INFORMATION:
| APPLICANT: TAN HEHIR, CRISTINA A. |
| APPLICANT: TAN HEHIR, CRISTINA A. |
| APPLICANT: TAN HEHIR, CRISTINA A. |
| APPLICANT: STATTEL, JAME R. |
| APPLICANT: STATTEL, JAMES M. |
| APPLICANT: BITONTI, ALAN R. |
| TILLE OF INVENTION: RC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REPERENCE: 08945.0003-00000 CURRENT FILING DATE: 2004-05-06 |
| PRIOR PILING DATE: 2004-05-06 |
| PRIOR PILING DATE: 2003-05-06 |
| RIOR FILING DATE: 2003-05-06 |
| SOFTWARE: Patentin Ver. 3.2 |
| SEQ ID NO 1 |
| LENGTH: 36 |
| TYPE: PRI |
| ORGANISM: Human immunodeficiency virus
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                                             100.0%; Score 36; DB 7; Length 145; 100.0%; Pred. No. 4.6e-29;
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                                                                                                 Indels
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                                                                                                                                            1 YTNTIYTLLEBSQNQOEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10841956A publication No. US20050281829A1 GENERAL INFORMATION:
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                                   Ouery Match
Best Local Similarity 100.
Matches 36; Conservative
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US-11-084-858-11
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US-11-029-003-1
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APPLICANT: Dannel, Inomas O.

APPLICANT: Hays, Anna-Maria
APPLICANT: Litzinger, David C.
APPLICANT: Litzinger, David C.
APPLICANT: Litzinger, David C.
APPLICANT: Litzinger, David C.
APPLICANT: Kimmel, Bruce E.
APPLICANT: Kimmel, Bruce E.
APPLICANT: Keefe, William M.
ITLE OF INVENTION: Acids
FILE REFERENCE: AMEX-0041.00US
FILE REFERENCE: AMEX-0041.00US
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: 60/590,035
PRIOR PILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: 60/599,035
PRIOR FILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
SEQ ID NO 22
LENGTH: 36
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Sequence 33, Application US/11112277

Sequence 33, Application US/11112277

Publication No. US20050267293A1

GENERAL INFORMATION:

APPLICANT: Bousquet-Gagnon, Nathalie

APPLICANT: Bridon, Dominique P.

TITLE OF INVENTION: CONJUGATES

FILE REFERENCE: 500862003700

CURRENT APPLICATION NUMBER: US/11/112,277

CURRENT PILING DATE: 2005-04-22

PRIOR FILING DATE: 2004-04-23

NUMBER OF SEQ ID NOS: 53

SOFTHARE: FSECSED FOR Windows Version 4.0

SEQ ID NO 33

LENGTH: 37
Query Match

75.0%; Score 27; DB 7; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 27; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                             10 EESQNQQEKNEQELLELDKWASLWNWF 36
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ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                Sequence 22, Application US/11187687
Sequence 22, Application US/11187687
Publication No. US20060019347A1
GENERAL INFORMATION:
APPLICANT: Cho, Ho Sung
APPLICANT: Daniel, Thomas O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: T20 Analogue
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ORGANISM: Artificial Sequence
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NAME/KEY: MOD_RES
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ORGANISM: Artificial Sequence
FATURE: Peptide
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
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Sequence 4, Application US/10841956A

Publication No. US2005021829A1

GENERAL INFORMATION:

APPLICANT: TAN HEHIR, CRISTINA A.

APPLICANT: PETERS, ROBERT T.

APPLICANT: STATTEL, JAMES M.

APPLICANT: BITONTI, ALAN R.

TILLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
FILE REFERENCE: 08945.0003-00000

CURRENT APPLICATION NUMBER: US/10/841,956A

CURRENT APPLICATION NUMBER: 60/468,835

PRIOR APPLICATION NUMBER: 60/468,835

PRIOR PILING DATE: 2003-05-06

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PATENTIN VOI: 3.2

SEQ ID NO 4

LENGTH: 267
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APPLICANT: MEZO, ADAM R.
APPLICANT: PETERS, ROBERT T.
APPLICANT: PALCMBELLA, VITO J.
APPLICANT: BIONTI, ALAN R.
TITLE OF INVENTION T.
FILE REFERENCE: 08945.0003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
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                                                                                                                                                               Query Match 75.0%; Score 27; DB 7; L. Best Local Similarity 100.0%; Pred. No. 1.2e-20; Matches 27; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 6.6e-20;
Matches 27; Conservative 0; Mismatches 0;
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                                                                                           ) ORGANISM: Human immunodeficiency virus US-11-187-687-24
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  SOFTWARE: Patentin version 3.3 SEQ ID NO 24 LENGTH: 44
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 8
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                                                                        TYPE: PRT
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APPLICANT: Milan, Troy Bavid C.
APPLICANT: Litzinger, David C.
APPLICANT: Maxiani, Roberto
APPLICANT: Keefe, William M.
TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
TITLE OF INVENTION: Adds
FILE REFERENCE: AMBX-0041.00US
CURRENT APPLICATION UNMBER: US/11/187,687
PRIOR PLING DATE: 2005-07-21
PRIOR PLING DATE: 2004-07-22
PRIOR APPLICATION NUMBER: 60/590,035
PRIOR PLING DATE: 2005-03-07
PRIOR APPLICATION UNMBER: 60/599,709
PRIOR APPLICATION UNMBER: 60/599,709
PRIOR PLING DATE: 2005-03-07
PRIOR PLING DATE: 2005-03-07
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                                                                                              Length 37;
                                                                                         Query Match
75.0%; Score 27; DB 7; L.
Best Local Similarity 100.0%; Pred. No. 9.9e-21;
Matches 27; Conservative 0; Mismatches 0;
; LOCATION: 37
; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-33
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Publication No. US20060019347A1
GENERAL INFORMATION:
APPLICANT: Cho, Ho Sung
APPLICANT: Daniel, Thomas O.
APPLICANT: Hays, Anna-Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Matches 27; Conservative
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DB 6; Length 281; 7e-20;

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TYPE: PRT

ORGANISM: Artificial Sequence

ORGANISM: Aptide

FEATURE: Peptide

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: construct
                                                                                                                                                                                                     Query Match 75.0%; Score 27; DB Best Local Similarity 100.0%; Pred. No. 7e-Matches 27; Conservative 0; Mismatches
                                                                                                                                                           US-10-841-956A-7
SEQ ID NO 7
LENGTH: 281
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                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: construct
US-10-841-956A-8
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
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APPLICANT: STATEL, ADMES M.
APPLICANT: PALCHERS, ROBERT T.
APPLICANT: PALCHERS, VITO J.
APPLICANT: PALCHER, VITO J.
APPLICANT: PALCHER, VITO J.
APPLICANT: BITOWIT, ALAN R.
TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945.0003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT FILING DATE: 2004-05-06
PRIOR PHING DATE: 2004-05-06
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN Ver. 3.2
SOFTWARE: PATENTIN VER. 3.2
ILENGTH: 270
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APPLICANT: STATTEL, JAMES M.
APPLICANT: STATTEL, JAMES M.
APPLICANT: PALOMBELLA, VITO J.
APPLICANT: BITONII, ALAN R.
ITILE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
FILE REPERRENCE: 08945.0003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT PILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: 60/468,835
NUMBER OF SEQ 4D NOS: 59
SOFTWARE: PALENTING PATE: 2003-05-06
NUMBER OF SEQ 4D NOS: 59
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Pred. No. 6.7e-20;
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100.0%; Pred. No. 6.7e-20;
tive 0; Mismatches 0;
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100.0%; Pred. No. v.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TAN HEHIR, CRISTINA A. APPLICANT: MEZO, ADAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TAN HEHIR, CRISTINA A. APPLICANT: MEZO, ADAM R.
                                        ORGANISM: Artificial Sequence FEATURE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                          27; Conservative
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Best Local Similarity
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Best Local Similarity
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US-10-841-956A-5
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US-10-841-956A-7
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FEATURE: Peptide
CPHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
                                                                                                                                                         APPLICANT: THE RELIES, ADAM R.
APPLICANT: MEZO, ADAM R.
APPLICANT: MEZO, ADAM R.
APPLICANT: PETERS, ROBERT T.
APPLICANT: PALOMBELLA, VITO J.
APPLICANT: BITONTI, ALAN R.
TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945.0003-000000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT APPLICATION NUMBER: 60/468,835
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN VET: 3.2
LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
75.0%; Score 27; DB 6; Length 282;
Best Local Similarity 100.0%; Pred. No. 7e-20;
Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 EESQNQQEKNEQELLELDKWASLWNWF. 282
10 EESÓNQOEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 EESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                            Sequence 6, Application US/10841956A Publication No. US20050281829A1 GENERAL INFORMATION:
                                                                                   US-10-841-956A-6
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APPLICANT: CHILKOTI, ASHUtOSH
TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
FILE REFERENCE: 4176-101 CIP
CURRENT APPLICATION NUMBER: US/11/053,100
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 69/812,382
PRIOR PILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR PILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.3
LENGTH: 354
TYPE: PRT
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                     Gaps
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TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
FILE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
FILE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
FILE OF INVENTION NUMBER: US/11/053,100
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 69/812,382
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                           FEATURE: Peptide

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

HOFTER INFORMATION: construct

CS-10-841-956A-9
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                                                                                                                                                                                                                                                                                      Query Match 75.0%; Score 27; 'DB 6; Length 293; Best Local Similarity 100.0%; Pred. No. 7.3e-20; Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1). .. (354)
; OTHER INFORMATION: PET15b-ELP4-60-EK-T20 peptide
US-11-053-100-27
                                                                                                                                                                                                                                                                                                                                                                                                                                              267 EESQNQOEKNEQELLELDKWASLWNWF 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 EESQNQQEKNEQELLELDKWASLWNWF 354
                                                                                                                                                                                                                                                                                                                                                                                                       10 EESQNQQEKNEQELLELDKWASLWNWF 36
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OTHER INFORMATION: Synthetic Construct
FEATURE:
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                                                                                      TYPE: PRT
ORGANISM: Artificial Seguence
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
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TYPE: PRT

ORGANISM: Artificial
FEATURE:

PEATURE:

NAME/KEY: MISC_FEATURE:

AME/KEY: MISC_FEATURE:

COTHER INFORMATION: SPI17b-ELP4-60-TEV(Q/Y)-T20 peptide

US-11-053-100-36

Query Match

Best Local Similarity 100.0%; Pred. No. 8.8e-20;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy 10 EESONQOEKNEOELLELDKWASLWNWF 36

Oy 10 EESONQOEKNEOELLELDKWASLWNWF 356

Db 330 EESONQOEKNEOELLELDKWASLWNWF 356

Search completed: March 6, 2006, 16:33:25
Job time: 10.3333 secs
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1.7	Biocceleration Ltd.	
GenCore version 5.1.7	(c) 1993 - 2006 Bio	
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March Run on:

6, 2006, 16:12:57; Search time 117.333 Seconds (without alignments) 134.809 Million cell updates/sec

US-09-809-060A-2 36 Title:

Perfect score:

1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36 Scoring table: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0

2443163 segs, 439378781 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

geneseqp1980s: geneseqp2004s: geneseqp2002s: A Geneseq 21:* 1: qenesemino Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

		de			SUMMARIES	
Result		Query				
No.	Score	Match	Length	8	QI	Description
٦	36	100.0	36	ю	AAY89837	Aay89837 Core poly
7	36	100.0	36	4	AAB54786	
m	36	100.0	36	4	AAB92245	Aab92245 Virus rel
4	36	100.0	36	4	AAB78238	Aab78238 Core poly
S	36	100.0	36	4	AAB78237	Aab78237 Core poly
9	36	100.0	36	4	AAU70180	Aau70180 HIV viral
7	36	100.0	36	4	ABB02830	Abb02830 Viral cor
89	36	100.0	36	4	ABB01245	Abb01245 Viral DP1
o,	36	100.0	36	4	ABB01244	Abb01244 Viral DP1
10	. 36	100.0	36	4	AAU13791	Aau13791 DP178-lik
11	36	100.0	36	4	AAU13790	Aau13790 DP178-lik
12	36	100.0	36	ഹ	AA018772	Aao18772 HIV gp41
13	36	100.0		Ŋ	ADE02850	_
14	36	100.0		ហ	ADE02716	Ade02716 Hybrid po
15	36	100.0		ø	ABO10164	Abo10164 HIV1-SF2
16	. 36	100.0		œ	ADN06923	
17	36	100.0		œ	ADS87258	
18	36	100.0		Φ	ADY71493	HIV-1
19	36	100.0	269	0	AAY22835	
20	36	100.0	269	7	AAY22834	
21	36	100.0	269	'n	ABG68305	Abg68305 Envelope
22	36	100.0	269	വ	ABG68306	
23	36	100.0	269	9	ABU57712	

	Abu63182 Protein # Abu63186 Env prote Ado26144 HIV env p Adx39689 HIV Env p Adx39689 HIV Env p Adx128706 env gene Adx29706 env gene Adx38790 ARV-2 (9B Add31868 HIV-1 pol Adw43070 HIV-1 gpl Adw43070 HIV-1 gpl
AAW33615 AAY77309 ABU57560 ABU63193 AAX05795 AAW77298 AAY77298 AAY77302 AAY77302 AAY77302 AAY77302	ABUG3182 ABUG3186 ABUZ3614 ABW31284 AAW31284 AARC3706 AARC3706 AARC3706 AAW43070 AAW43070
2275 2275 2275 2275 32275 32275 3322 3322	8 8 8 8 8 8 5 5 5 6 6 6 6 6 6 6 6 6 6 6
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2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

AAY89837

AAY89837 standard; peptide; 36 AA.

AAY89837;

23-MAY-2000 (first entry)

Core polypeptide fragment T No. 1406.

Retrovirus, hybrid polypeptide, enhancer, gp41, envelope protein, HIV-1, HIV-2, SIV, pharmacokinetic, half-life, growth factor, cytokine, viral, anti-fusogenic, differentiation factor, interleukin, interferon, colony stimulating factor; hormone; angiogenic factor.

Unidentified

WO9959615-A1.

25-NOV-1999.

99WO-US011219. 20-MAY-1999; 98US-00082279. 20-MAY-1998;

(TRIM-) TRIMERIS INC.

Lambert DM, Anwer MK, Merutka G, Barney S, Guthrie KI,

WPI; 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence.

Disclosure; Page 45; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (1941) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or prevention of a disease. The core polypeptides are bloactive peptides selected from a growth factor, cytokine, differentiation factor, interferon, colony stimulating factor, hormone or anglogenic

Abu57713 Human imm

6 ABU57713

269

36 100.0

24

peptidase or protease degradation. This minimises the need for more frequent, or even continual, administration of the peptides. AAB54784 to AAB55431 represent peptides used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

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The present invention describes a modified anti-viral peptide (I)

comprising a peptide that exhibits anti-viral activity and a reactive

comprising a peptide that exhibits anti-viral activity and a reactive

group which is reactive with amino groups, hydroxyl groups, or thiol

groups on blood components to forms stable covalent bonds. (I) has anti-

viral and anti-fusogenic activities. (I) inhibits viral infection of

cells by inhibiting cell-cell fusion or free virus infection or to reduce

cells by inhibiting cell-cell fusion or free virus infection or to reduce

the level of membrane fusion events between two or more entities, e.g.,

virus-cell or cell-cell, relative to the level of membrane fusion that

coccurs in the absence of the peptide. (I) is useful in the treatment of

patients who are suffering from viral infection, e.g. HIV, RSV, HBIV,

MeV, and SIV. (I) may be administreed prophylactically to previously

uninfected individuals. This is useful in cases where an individual has

components of the blood, such as immunoslobin, serum albumin, red

lived components of the activity is extended for days to weeks.

This is due to improved stability in vivo and a reduced susceptibility to
                                                                                                                                                                                                           ö
                     infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides
  factor. The peptides of the invention can be used for inhibiting viral
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Long lasting fusion peptide inhibitor; viral infection; antiviral; antifusgeant; moballe blood component; measles virus; MeV; SIV; sinian immunodeficiency virus; human parainfluenza virus; HPIV; RSV; human respiratory syncytial virus; human immunodeficiency virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A modified peptide and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds useful for treatment of viral infections, e.g.
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                                                                                                                                                                  Length 36;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robitaille M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV antiviral activity exhibiting peptide SEQ ID NO:3.
                                                                                                                                                              100.0%; Score 36; DB 3; I
100.0%; Pred. No. 3.3e-27;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                               1 YTNTIYTLLEESONOOEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                              1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boudjellab N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 173; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        AAB54786 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human immunodeficiency virus.
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99US-0153406P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                      36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-007496/01.
                                                                                                                                                                                 Local Similarity
                                                                                                                        Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200069902-A1
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10-SEP-1999;
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05-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAB54786;
                                                                                                                                                                Query Match
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The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a
reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
a less therapeutically active amino acid region (IV), which covalently
bonds with amino/hydroxyl/thiol groups on blood components to form a
peptidase stabilised therapeutic peptide components to form a
(I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity in
vivo for the treatment of various disorders. Endogenous therapeutic
peptides are not suitable as drug candidates as they require frequent
administration due to rapid degradation by peptidases in the body.
Modifying and attaching therapeutic peptides to albumin prevents or
reduces the action of peptidases to increase length of activity (half
life) and specificity as bonding to large molecules decreases
ABB90829 to AAB9241 represent peptides which can be used in the
exemplification of the present invention
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl; thiol; hormone, growth factor, neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thibaudeau K;
                                                                                                                Length 36;
                                                                                                                                               Indels
                                                                                                                                                  ö
                                                                                                                Score 36; DB 4; ]; Pred. No. 3.3e-27; 0; Mismatches 0;
                                                                                                                                                                               1 YTNTIYTLLEBSQNQOEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                    YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes
                                                                                                                                                                                                                                                                                                                                                                                                 Virus related peptide SEQ ID NO:1421.
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                                                                                                                                                                                                                                                                                                   ż
                                                                                                                                                                                                                                                                                                AAB92245 standard; peptide; 36
                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 36; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0134406P.
99US-0153406P.
99US-0159783P.
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                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112059/12.
                                                                                 Sequence 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                AAB92245;
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                                                                                                                                                                  The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide. The hybrid and core polypeptides can be used for modulating fusogenic events and intracellular processes involving coiled coil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperme egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus, respiratory sprivial infections caused by human immunodeficiency virus, respiratory surginal coiled-coil beat virus, hepatitis B virus, Mason-Pfizer virus and polio virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Core polypeptide, enhancer, antiviral, anti-HIV, virucide, hepatotropic, antiinflammatory, hybrid polypeptide, colled-coil peptide interaction, fusion-related disorder; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             efficacy and minimies the incidence and severity of adverse side effects. In addition, this increases the sensitivity of the diagnostic
                                                              Gaps
                                                              ;
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Query Match
100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 36; Conservative 0; Mismatches 0: The servative conservative of Mismatches or the servative conservative of Mismatches or the servative conservative or Mismatches or the servative conservative conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lambert DM;
                                                                                                           1 YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                        1 YINTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 58; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merutka G,
                                                                                                                                                                                                                                                                                     AAB78238 standard; peptide; 36 AA
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Core polypeptide T1406.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TRIM-) TRIMERIS INC.
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                                                                                                                                                                                                                                                                                                                                                                                            19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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                                                                                                                                                                                                                                                                                                                                          AAB78238;
                                                                                                                                                                                                                                                           RESULT 4
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The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide. The hybrid and core polypeptides can be used for modulating fusogenic events and intracellular processes involving colledcoil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg fusion), intracellular processes involving colled-coil peptides (e.g. bacterial infections) and viral infections caused by human immunodeficiency virus, respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and polio virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the increases the severity of adverse side effects. In addition, this increases the sensitivity of the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic; antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lambert DM;
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1 YINTIYTLEESQNQOEKNEQELLELDKWASLWNWF 36
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100.0%; Pred. No. 3.3e-27;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 58; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merutka G,
                                                                                                                                                                                                      AAB78237 standard; peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                              19-APR-2001 (first entry)
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
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RESULT 6

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Gaps

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Query Match Best Local Similarity

Matches

virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;

Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;

Viral core polypeptide, SEQ ID NO: 1357.

(first entry)

(revised)

06-AUG-2003 03-JAN-2002

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The invention relates to methods of generating immunogens that elicit

neutralising antibodies which target regions of viral envelope proteins

such as the gg120/gg41 (glycoprotein 120/glycoprotein 41) complex of HIV-

1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and

AAU70677-AAU70743 represent stabilising peptides modelling the alpha-

ca AAU70677-AAU70743 represent stabilising peptides modelling the alpha-

ca AAU70677-AAU70743 represent stabilising peptides modelling the alpha-

catabilise fusion-active intermediate structures, which can be used as

caccine immunogens. Immunogenic compositions comprise a viral envelope

catabilise fusion and entry, and optionally, a viral cell surface receptor or

control fusion and entry, and optionally, a viral cell surface receptor or

its fragment. The stabilising peptide is capable of associating with the

carvelope protein or its fragment to form a stabilised, fusion active

carvelope protein or its fragment to form a stabilised, fusion active

carvelope protein or its fragment to form a stabilised, fusion active

carvelope protein or its fragment to form a stabilised, fusion active

carvelope protein or its fragment to form a stabilised, fusion active

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carvelope protein or its fragment to form a stabilised active

carvelope protein or its fragment to form a stabilised active

carvelope protein or its fragment are used to determine the ability of immunogen various forms of antibody response raised against HIV-1 gp41 domains. The sequences and

carvelope are useful for inhibiting HIV infection, for inducing an immune immune in an animal and for raising antibodies
                                                                                                                                                                                             Human, HIV-1, human immunodeficiency virus; gp41; glycoprotein 41; gp120;
anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
alpha-helical region; ectodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic composition for inhibiting HIV infection, comprises viral envelope protein or its fragment exterior to viral membrane, a stabilizing peptide, and, optionally, viral cell surface receptor or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 36; DB 4; Length 36; 100.0%; Pred. No. 3.3e-27; ive 0; Mismatches 0; Indels
                                                                                                                                             HIV viral envelope protein stabilising peptide #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 45; 84pp; English.
AAU70180 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-2001; 2001WO-US008108.
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                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PANA-) PANACOS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wild CT, Allaway GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-626098/72.
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                                                                                                                                                                                                                                                                                                                                       WO200170262-A2
                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                               14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001.
                                               AAU70180;
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Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus

Disclosure; Page 524; 587pp; English.

infection

'n,

Erickson JB, Lambert DM,

Delmedico MK,

Antczak JB,

WPI; 2001-514829/56

(TRIM-) TRIMERIS INC.

07-FEB-2001; 2001WO-US003988. 29-FEB-2000; 2000US-00515965.

WO200164013-A2.

Infection

Viruses.

07-SEP-2001.

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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 588-595 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with apptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-HUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 36;
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100.0%; Pred. No. 3.3e-27;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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06-AUG-2003
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Viruses.

ABB02830 standard; peptide; 36 AA

11-SEP-2003 (revised)

ABB02830;

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Gaps

Sista P;

Lambert DM,

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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-555 (heptad repeat region RR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV specification. The present sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SBP-2003 to street OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex.
                                                                                                                                                                                 Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-retroviral, DP178-like, DP107-like, transmembrane protein gp41; antifusogenic, antiviral, HIV transmission; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 36; DB 4; 100.0%; Pred. No. 3.3e-27;
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                                                                                                     Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP178-like/DP107-like peptide T-1406
                                                                                                                                                                                                                                                                    Disclosure; Page 58; 587pp; English.
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                     29-FEB-2000; 2000US-00515965
                                                                                                     Delmedico MK,
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                                                             (TRIM-) TRIMERIS INC.
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                                                                                                     Antczak JB,
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                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-LIAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides darived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV specification. The present sequence is a peptide provided in the specification. (Updated on 06-MUG-2003 to correct OS field.) (Updated on 11-SSP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                  Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus, HIV, respiratory syncytial virus, RSV, virucide, heptad repeat region, transmembrane protein, gp41, HR1, HR2,
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                                                                                                                                                                                                        Sista
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                                                                                                                                                                                                      Lambert DM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 36; DB 4; 1 100.0%; Pred. No. 3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                  Antczak JB, Delmedico MK, Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 58; 587pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB01244 standard; peptide; 36 AA
                                                                              07-FEB-2001; 2001WO-US003988
                                                                                                                      29-FEB-2000; 2000US-00515965
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/note=
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                                                                                                                                                            (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                            WPI; 2001-514829/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36 AA;
WO200164013-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200164013-A2
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                                      07-SEP-2001,
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06-AUG-2003
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                                                                                                                                                                                                                                                                                                                               infection.
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Matches

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Length 36; Indels Merutka G;

Viruses.

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The present all products which exhibite control calls the present all present all presents are controlled to the control calls of the present all calls be petides. The peptides of the transmembrane protein gp41 from human calls 639-673 of the transmembrane protein gp41 from human calls 639-673 of the transmembrane protein gp41 from human calls saled to amino acids 538-595 of gp41 from HIV-LIAI. The phtide corresponds to amino acids 558-595 of gp41 from HIV-LIAI. The invention of a lor relates to a method of identifying compounds that inhibit the corresponds to amino acids 558-595 of gp41 from HIV-LIAI. The invention of correcting the formation of a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or beence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, cantivitied or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to unlinfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 36; DB 4; Length 36; 100.0%; Pred. No. 3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                       present invention relates to peptides which exhibit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1; isolate LAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP178-like/DP107-like peptide T-1405.
                                     Disclosure; Page 77; 259pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TRIM-) TRIMERIS INC
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Disclosure; Page 77; 259pp; English.

DP107/DP178 complex.,

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            The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU1409) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex. The method comprises absence of a test compound, in a reaction mixture containing DP107 and small molecule compounds, which may themselves exhibit antifusogenic, and invitate of interfall for interacellular modulatory activity. The DP178-like/DP107-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method of treating an HIV infection in an individual, which involves administering in combination a chemokine co derepetor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its derivative. Other viral infections can also be treated using the method. The present sequence is a peptide derived from HIV and useful in the method of the invention
                                                                                                                                                                                                                                                                    peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treatment of HIV infection in an individual involves administration of a combination of chemokine co-receptor five antagonist and a specified HIV
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                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
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100.0%; Pred. No. 3.3e-27;
:ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               envelope polypeptide.
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                                                                                                                                                                                                                                                                                                                                                     Sequence 36 AA;
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1 YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                                           RESULT 14
                                                                                                    The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WGEWEGKI or WASLWEWF. The enhancer includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel peptide sequence enhances pharmacokinetic properties of any core polypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging tructures in vivo. The novel polypeptide and hybrid polypeptides are useful for modulating fusogenic events and exhibit antifusogenic or antiviral activity. The novel hybrid polypeptide is useful for decreasing viral infection and modulating intracellular processes involving coiledcoil peptide interactions. The novel hybrid polypeptide comprises insulin or its fragment, so the core polypeptide is useful for ameliorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also useful as a part of prognosis for preventing disorders including fusion the context and viral infection and modulating the preventing disorders including fusion useful as a part of prognosis for preventing disorders including fusion fevents and viral infection and including the context and viral infection and modulating coiledcover.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybrid, enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
pharmacokinetic; fusogenic; insulin; diabetes.
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     DB 5; Length 36;
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                                                   Indels
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  100.0%; Score 36; DB 5; 1 100.0%; Pred. No. 3.3e-27;
                                                                                                                                    YINTIYILEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                   0; Mismatches
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Query Match
Best Local Similarity
Matches 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2004
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                                                                                                                                                                                                                                                                                                                              ADE02850;
                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                   ADB02850
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ADBC
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The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WGEWEGKI or WASLWEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel hybrid polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core peptide sequence enhances plantamacokinetic properties of any core polypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging are useful for example, a polypeptide and hybrid polypeptides are useful for modulating fusogenic events and exhibit antifusogenic or antiviral activity. The novel hybrid polypeptide is useful for decreasing viral infection and modulating intracellular processes involving colleducing the refractions. The novel hybrid polypeptide is useful for amellorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also events and viral infection that involves cell-cell and/or virus-cell infection, and for diagnosis and in vivo inmaging methods. This sequence represents an enhancer peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein sequences linked to core polypeptide e.g. therapeutic protein.
                                                                                                                                                                                                                                                                                                             hybrid, enhancer, anti-fusogenic, antiviral, virucide, antidiabetic, pharmacokinetic, fusogenic, insulin, diabetes.
                                                                                                                                                                                                                                Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Residue is modified by acetyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambert DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anwer MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 1223; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merutka G,
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ADE02716 standard; peptide; 36
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                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TRIM-) TRIMERIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-424396/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-1998;
                                                                                                                                                      29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2002
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                                                                             ADE02716;
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Gaps

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Indels

Length 36;

100.0%; Score 36; DB 5; L 100.0%; Pred. No. 3.3e-27; ive 0; Mismatches 0;

36, Conservative

Matches

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Gaps

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100.0%; Score 36; DB 5; Length 36; 100.0%; Pred. No. 3.3e-27; ive 0; Mismatches 0; Indels

36; Conservative

Matches

Local Similarity

Query Match

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Best Local Similarity

Query Match

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Inhibiting transmission of Epstein-Barr virus to a cell, by contacting the cell with a peptide consisting of a region of Epstein-Barr virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
Epstein-Barr virus infection; heptad repeat motif.
1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1; isolate SF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petteway SR;
                                                                                                                                                                                                                                                                                                                                                          HIV1-SF2 gp41 protein, DP85 peptide.
                                                                                                                                               ABO10164 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00073028.
94US-00255208.
94US-00360107.
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                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lambert DM,
                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TRIM-) TRIMERIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-465599/44.
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07-JUN-1994;
20-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6518013-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                      23-OCT-2003
19-AUG-2003
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                                                                                                                                                                                                          AB010164;
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                                                                                       RESULT 15
                                                                                                                AB010164

DECOUNTY

AB0101
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The invention relates to inhibiting (M) transmission of an Epstein-Barr virus to a cell, comprising contacting the cell with an effective concentration of a peptide consisting of a region of 16.39 consecutive camino acids of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of ALLMOTIS.

107x178x4 or PLZIP sequence search motifs, the peptide further comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic group, or macromolecular carrier group, and group, hydrophobic group, or macromolecular carrier group, and chain of the virus to the cell is inhibited. The peptides were identified by analysing the structure/motifs present in the HIV-1 glycoprotein 41 anit-HIV peptides DPL07 and DP178. These heptad repeat motif containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic organisms and HIV isolates, looking for DPL07/178 structural analogues. The method is useful for inhibiting transmission of Epstein-Barr virus to a cell and Epstein-Barr virus infection. The present sequence is a control peptide used in the study of the DP178 stucture. (Updated on 23-correct) corrected on 23-correct organisms and HIV isolates, etclein the DP178 stucture. Example; Fig 1; 716pp; English.

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ch 100.0%; Score 36; DB 6; Length 36; Similarity 100.0%; Pred. No. 3.3e-27; 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                   YTYTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                          1 YTNTIYTLLEESONOOEKNEOELLELDKWASLWNWF 36
                                                       Local Similarity
Sequence 36 AA;
                                        Query Match
                                                              Best Loca
Matches
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Gaps .; 0

6, 2006, 16:19:04 Search completed: March Job time : 118.333 secs

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RESULT 2
US-11-029-003-1
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                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                             March 6, 2006, 15:50:56 ; Search time 10 Seconds
    (without alignments)
    72.002 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34
Sequence 4,
Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10
Sequence 7,
Sequence 5,
Sequence 11,
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Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                          Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                     198
1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-841-956A-1
US-11-187-67-22
US-11-112-277-33
US-11-187-687-24
US-11-187-687-24
US-11-0506-796A-5
US-10-506-796A-5
US-10-506-796A-5
US-10-506-796A-6
US-10-506-796A-6
US-10-506-796A-6
US-10-506-796A-6
US-11-12-277-34
US-11-112-277-34
US-11-112-277-6
US-11-112-277-6
US-11-112-277-6
US-11-112-277-6
US-11-112-277-6
US-11-112-277-6
US-11-112-277-6
US-11-112-277-6
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-112-277-36
                                                                                                                                                                                    135346 seqs, 20000420 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            protein search, using sw model
                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                           US-09-809-060A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length
                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 50
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                                                                      Sequence 8659, Ap Sequence 103, App Sequence 103, App Sequence 7039, Ap Sequence 102, App Sequence 102, App Sequence 6943, App Sequence 6943, App Sequence 3776, App Sequence 12581, App Sequence 12581, App Sequence 101, App Sequence 3966, App
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                                                          Sequence
                    Sequence
Sequence
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Publication No. US20050260194A1
GENERAL INFORMATION
APPLICANT: PETERS, ROBERT T.
APPLICANT: RIVER, DANEL S.
APPLICANT: STATTEL, JAMES
TITLE OF INVENTION: INWUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
FILE REPERENCE: 08945.0007-01000
CURRENT APPLICATION NUMBER: US/11/029,003
CURRENT APPLICATION NUMBER: US/311/029,003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PETERS, ROBERT T.
APPLICANT: PETERS, ROBERT T.
APPLICANT: PETERS, ROBERT T.
APPLICANT: STATEL, JAMER M.
APPLICANT: PALOMBELLA, VITO J.
APPLICANT: BITONII, ALAN R.
TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REPERENCE: 08945,0003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT PILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR APPLICATION NUMBER: 5003-05-06
SOFTWARE OF SEQ ID NOS: 59
SOFTWARE PATENTIN Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 36;
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88.9%; Score 176; DB 6;
Best Local Similarity 86.1%; Pred. No. 1.7e-15;
Matches 31; Conservative 4; Mismatches 1.
                                                                                                                                                                                                                                                                                                                     US-11-045-024-12581
                                                                                                                                                                                                                                                                                                                                                           US-11-045-024-3966
US-11-045-024-3969
                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10841956A Publication No. US20050281829A1 GENERAL INFORMATION: APPLICANT: TAN HEHIR, CRISTINA A.
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APPLICANT: Hays, Anna-Maria
APPLICANT: Hays, Anna-Maria
APPLICANT: Wilson, Troy E.
APPLICANT: Litzinger, David C.
APPLICANT: Litzinger, David C.
APPLICANT: Litzinger, David C.
APPLICANT: Kimmel, Bruce E.
APPLICANT: Kimmel, Bruce E.
APPLICANT: Keefe, William M.
TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
TITLE OF INVENTION: Acids
FILE REFERENCE: AMBX-0041.00US
TITLE OF INVENTION: Acids
FILE REFERENCE: AMBX-0041.00US
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: 60/590,035
PRIOR FILING DATE: 2005-07-07
PRIOR FILING DATE: 2005-07-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
SEQ ID NO 24
LENGTH: 44
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                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD_RES
LOCATION: 37
COTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-1277-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 88.9%; Score 176; DB 7; Best Local Similarity 86.1%; Pred. No. 1.7e-15; Matches 31; Conservative 4; Mismatches 1
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Best Local Similarity 86.1%; Pred. No. 2e-15;
Matches 31; Conservative 4; Mismatches
     CURRENT APPLICATION NUMBER: US/11/112,277
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/565,228
PRIOR FILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-11-187-687-24
Sequence 24, Application US/11187687
Publication No. US20060019347A1
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Sequence 10, Application US/11089426
Publication No. US20050261229A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen D.
APPLICANT: Lo, Kin-Ming
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: T20 Analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cho, Ho Sung
APPLICANT: Daniel, Thomas O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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US-11-187-687-22
| Sequence 2.2, Application US/11187687
| Publication No. US20060019347A1
| GENERAL INFORMATION:
| APPLICANT: Cho, Ho Sung
| APPLICANT: Cho, Ho Sung
| APPLICANT: Hays, Anna-Maria
| APPLICANT: Misson, Troy E.
| APPLICANT: Misson, Troy E.
| APPLICANT: Mariani, Roberto
| MINBER OF FILING DATE: 2004-07-21
| PRIOR FILING DATE: 2005-03-07
| NUMBER OF SEQ ID NOS: 28
| SOFFWARE: PatentIn version 3.3
| SOFFWARE: PatentIn version 3.3
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Pred. No. 1.7e-15;
4; Mismatches 1; Indels
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Sequence 33, Application US/11112277
Publication No. US20050267293A1
GENERAL INFORMATION:
APPLICANT: Bousquet-Gagnon, Nathalie
APPLICANT: Quraishi, Omar
APPLICANT: Bridon, Dominique P.
TITLE OF INVENTION: CONJUGATES
TITLE OF INVENTION: CONJUGATES
FILE REFERENCE: 500862003700
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                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human immunodeficiency virus
PRIOR APPLICATION NUMBER: 60/539,207
PRIOR FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: 60/487,964
PRIOR FILING DATE: 2003-07-17
PRIOR PLING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 1
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                              ch 88.9%;
1 Similarity 86.1%;
31; Conservative 4
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Best Local Similarity
Matches 31; Conserv
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LENGTH: 36
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Publication No. US20060013831A1
GENERAL INFORMATION:
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                 TITLE OF INVENTION: For Fusion Proteins For Enhancing the Immunogenicity of TITLE OF INVENTION: Protein and Peptide Antigens FILE REFERENCE: LEX-007

CURRENT APPLICATION NUMBER: US/11/089,426

CURRENT FILING DATE: 2005-03-24

PRIOR APPLICATION NUMBER: US/09/621,268

PRIOR FILING DATE: 1999-07-21

PRIOR PILING DATE: 1999-07-21

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 10
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APPLICANT: MATOBA, Nobuyuki
APPLICANT: ARNTZEN, Charles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.000602
CURRENT APPLICATION NUMBER: US/10/506,796A
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; OTHER INFORWATION: HIV-1 isolate 1924v3.20 (residues 649-685)
US-10-506-796A-7
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:Fused OTHER INFORMATION: polypeptide from pdC-muFC vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 164; DB 7; Length 44;
Pred. No. 6e-14;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 69.7%; Score 138; DB 6; Length 36; 1 Similarity 96.0%; Pred. No. 7.3e-11; 24; Conservative 1; Mismatches 0; Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US03/07073
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
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; Publication No. US20060013831A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.8%;
90.6%;
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Seguence
Wesolowski, John
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Best Local Similarity 90.6
Matches 29; Conservative
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Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: PEPTIDE
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US-10-506-796A-7
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Sequence 1, Application US/10506796A

Sequence 1, Application US/10506796A

Publication No. US20060013831A1

GENERAL INFORMATION:

APPLICANT: MATOBA, Nobuyuki

APPLICANT: MATOBA, Nobuyuki

APPLICANT: ARNTZEN, Charles

TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE

TITLE REFERENCE: 01231.0006U2

CURRENT APPLICATION NUMBER: US/10/506,796A

CURRENT APPLICATION NUMBER: 0504-09-03

PRIOR FILING DATE: 2003-03-06

PRIOR FILING DATE: 2002-03-06

PRIOR FILING DATE: 2002-03-06

PRIOR FILING DATE: 2002-03-06

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 9

SEQ ID NO 1

FUNDANTION 1
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APPLICANT: ARNTZEN, Charles
TTLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.0006U2
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2004-09-03
PRIOR FULING DATE: 2003-03-06
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-03-06
SOFTWARE: PATENTION NUMBER: 60/362,247
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTION OF SEQ ID NOS: 9
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LOCATION: (1)...(35)
CATHEN INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
NS-10-506-796A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(36)
; OTHER INFORMATION: HIV-1 isolate 593 clone (residues 649-685)
US-10-506-796A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 36;
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Pred. No. 9.7e-11;
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
PRATURE: PEPTIDE
LOCATION: (1)..(36)
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Best Local Similarity 96.0%;
Matches 24; Conservative
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Gaps
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Publication No. US20050260194A1
GENERAL INFORMATION:
APPLICANT: PETERS, ROBERT T.
APPLICANT: RIVERA, DANIEL S.
APPLICANT: BITONIT, ALAN J.
APPLICANT: BITONIT, ALAN J.
APPLICANT: BITONIT, JAMES
TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
FILE REPREMEER: 0845.0007-01000
CURRENT APPLICATION NUMBER: US/11/029,003
CURRENT PILING DATE: 2005-01-05
FRIOR PRILING DATE: 2004-01-26
PRIOR PELICATION NUMBER: 60/487,964
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/469,600
PRIOR APPLICATION NUMBER: 60/469,600
PRIOR APPLICATION NUMBER: 60/469,600
PRIOR APPLICATION NUMBER: 60/469,600
SRIOR APPLICATION NUMBER: 60/469,600
            APPLICANT: PALOWBELLA, VITO J.
APPLICANT: BILONTI, ALAN R.
FILLE OF INVENTION: FC CHIMBERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945.0003-00000, CURRENT APPLICATION NUMBER: US/10/841,956A, CURRENT FILING DATE: 2004-05-06, PRIOR APPLICATION NUMBER: 60/468,835 PRIOR APPLICATION NUMBER: 60/468,835 PRIOR PLING DATE: 2003-05-06, NUMBER OF SEQ ID NOS: 59 SOFTWARE: Patentin Ver. 3.2 SEQ ID NO 3
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Publication No. US20050267293A1
GENERAL INFORMATION:
APPLICANT: Bousquet-Gagnon, Nathalie
APPLICANT: Quraishi, Omar
APPLICANT: Bridon, Dominique P.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
TITLE OF INVENTION: CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.6%; Score 124; DB 6; Best Local Similarity 71.9%; Pred. No. 4.1e-09; Matches 23; Conservative 3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 124; DB 7;
Pred. No. 4.1e-09;
3; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Human immunodeficiency virus US-10-841-956A-3
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Best Local Similarity 71.9%;
Matches 23; Conservative
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| Publication No. US20060013831A1
| GENERAL INFORMATION:
| APPLICANT: MATOBA, Nobuyuki
| APPLICANT: ARNTZEN. Charles
| APPLICANT: ARNTZEN. Charles
| TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
| TITLE OF INVENTION: COMPOSITION NUMBER: US/10/506,796A
| CURRENT APPLICATION NUMBER: PCT/US03/07073
| PRIOR APPLICATION NUMBER: PCT/US03/07073
| PRIOR APPLICATION NUMBER: 60/36,247
| PRIOR FILING DATE: 2002-03-06
| PRIOR PILING DATE: 2002-03-06
| PRIOR FILING DATE: 2002-03-06
| PRIOR PLOR PRESENCE: DOS: 9
| SOFTWARE: Patentin Version 3.2
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                      APPLICANT: MATOBA, Nobuyuki
APPLICANT: ARNTER, Chearles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 0.1231.0006U2
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2.004-0.9-03
PRIOR APPLICATION NUMBER: PCT/US03/07073
PRIOR FILING DATE: 2.003-0.3-06
PRIOR FILING DATE: 2.003-0.3-06
PRIOR FILING DATE: 2.003-0.3-06
SEQ ID NOS: 9
SOFTWARE: PLACE OF SEQ ID NOS: 9
SOFTWARE: PACENTIN VEYSION 3.2
SEQ ID NO 3
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COTHER INFORMATION: HIV-1 isolate 98BRRS012 (residues 649-685)
US-10-506-796A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 135; DB 6;
Pred. No. 1.7e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.2%; Score 133; DB 6 Best Local Similarity 92.0%; Pred. No. 3e-10; Matches 23; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human immunodeficiency virus type 1
US-10-506-796A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQTQQEKNEQELLELDKWASLWNWF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 SONQOEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
APPLICANT: MOR, TBafrir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
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US-10-506-796A-6
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US-10-841-956A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Sequence 4, Application US/10506796A

Publication No. US20060013831A1

REBERAL INFORMATION:
APPLICANT: MATCBA, Nobuyuki
CURENT MATCAN: CAPALES
CURRENT APPLICATION NUMBER: US/10/506,796A

CURRENT FILING DATE: 2004-09-03
PRIOR FILING DATE: 2003-09-03
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1) .:(35)
COTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
US-10-506-796A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
62.6%; Score 124; DB 7; Length 40;
Best Local Similarity 71.9%; Pred. No. 4.2e-09;
Matches 23; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.1%; Score 123; DB 6; Length 36;
88.0%; Pred. No. 5e-09;
                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
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FILE REFERENCE: 500862003700
CURRENT APPLICATION NUMBER: US/11/112,277
CURRENT FILING DATE: 2005-04-22
FRIOR APPLICATION NUMBER: US 60/565,228
FRIOR FILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 SONOGEKNEGELLELDKWASLWNWF 36
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Job time : 11 secs
                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: T1249 Analogue
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 88.0
Matches 22; Conservative
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NAME/KEY: MOD_RES
LOCATION: 40
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NAME/KEY: PEPTIDE
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; TITLE OF INVENTION: USING COMBINATORY THERA; FILE REFERENCE: 7872-036; CURRENT APPLICATION NUMBER: US/10/252,136; CURRENT FILING DATE: 2002-09-20; PRIOR APPLICATION NUMBER: US/08/973,952; PRIOR FILING DATE: 1998-05-29; NUMBER OF SEQ ID NOS: 82; SOFTWARE: Patentin Ver: 2.0; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Appl
                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, A
Sequence 38, Sequence 38, Sequence 3, A
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Sequence 13
Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                         Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                        198
1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-809-060-2
US-10-252-116-3
US-10-257-682-3
US-10-267-682-3
US-10-267-682-3
US-10-663-589-38
US-10-663-589-38
US-10-168-295-3
US-10-950-010-3
US-10-950-010-3
US-10-950-010-3
US-10-950-010-3
US-10-950-010-3
US-10-951-641-47
US-10-685-801-47
US-10-685-801-47
US-10-685-801-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-950-010-540
US-09-809-060-3
                                                                                                                                                                                                                  1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                           US-09-809-060A-2
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Match Length DB
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Sequence 4, Appli Sequence 1358, Ap Sequence 1359, Ap Sequence 4, Appli Sequence 39, Appli Sequence 39, Appli Sequence 4, Appli Sequence 142, Appli Sequence 1421, Appli Sequence 1421, Appli Sequence 1515, Appli Sequence 1515, Appli Sequence 1615, Appli Sequence 1615, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	mmunogens that Blicit against Fusion-Active Proteins	ength 36; Indels 0; Gaps NCY VIRUS AND OTHER
US-10-252-136-4 US-10-351-641-1358 US-10-267-682-4 US-10-267-682-4 US-10-267-582-3 US-10-667-582-39 US-10-671-282-39 US-10-671-282-39 US-10-671-282-39 US-10-950-010-4 US-10-950-010-4 US-11-066-697-1422 US-11-066-697-1422 US-10-950-010-541 US-10-950-010-541 US-09-809-060-85 US-09-809-060-85 US-09-809-060-85 US-09-809-060-85 US-09-809-779-451-5 US-09-814-628-1	LIGNMENTS enerating 1 Antibodies V Envelope 809,060 9,981	core 198; DB 3; L red. No. 6.6e-16; Mismatches 0; LLELDKWASLWNWF 36 LLELDKWASLWNWF 36 General Standard
	-2 Application US/09809 No. US20020010317A1 ON US20020010317A1 ON USAD ON US NO. USAD ON US USAD ON US USAD ON US U	larity 100.0%; Conservative TIYTLLEESQNQDEKN TIYTLLEESQNQDEKN TIYTLLEESQNQDEKN TIYTLLEESQNQDEKN TION: ROSS MDET, Dennis M. TION: TREATMENT TION
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	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	in Signature in Si
11778888888888888888888888888888888888	SULT 1 -09-809-060-2 Sequence 2, Application US/09809060 Bublication No. US20020010317A1 GENERAL INFORMATION: APPLICANT: Wild, Carl T. APPLICANT: Allaway, Graham P. TITLE OF INVENTION: Neutralizing A. TITLE OF INVENTION: Regions 6 HIV FILE REFERENCE: 1900.026001 CURRENT APPLICATION NUMBER: US/09/8 CURRENT APPLICATION NUMBER: US/09/8 CURRENT FILING DATE: 2000-03-17 NUMBER OF SEQ ID NOS: 87 SSO THANE: PATENTIN VERSION 3.0 LENGTH: 36 TYPE: PRT ORGANIEM: Human immunodeficiency v. 00RGANIEM: Human immunodeficiency v.	Query Match Best Local Similarity 100.0%; P Matches 36; Conservative 0; I YTHTIVILLESQUQQEKNEQE
2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-809-060-2 Sequence 2, A Publication N GENERAL INFOR APPLICANT: W APPLICANT: W TITLE OF INV	Query Match Best Local Si Matches 36; Qy 1 Y Db 1 Y Db 1 Y Sequence 3, P Publication N GENERAL INFOR APPLICANT: TITLE OF INV TITLE OF INV
	E) the transfer the transfer to the	0 0 80

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Sequence 3, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
Matthews, Thomas J.
Matthews, Thomas J.
Maid, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                   COMPUTER: INDEPTOR OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 198; DB 4; Length 36; 100.0%; Pred. No. 6.6e-16; ive 0; Mismatches 0; Indels
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IIP: 10036-2711

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMISSION
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 100.
Matches 36; Conservative
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                                                             COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Merutka, G.
APPLICANT: Merutka, G.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYBEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYBEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRE: US/10/351,641
FILE REFERENCE: 7872-100
CURRENT FILING DATE: 1999-07-09
PRIOR PAPLICATION NUMBER: 09/350,641
PRIOR PAPLICATION NUMBER: 09/315,304
PRIOR PILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SSDCTMARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                           Length 36;
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                                                                                                                                                        Query Match
100.0%; Score 198; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              100.0%; Score 198; DB 4;
100.0%; Pred. No. 6.6e-16;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                              TYPE: PRT
ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TILE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1357, Application US/10351641 Publication No. US20030186874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Core polypeptide US-10-351-641-1357
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GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
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; Publication No. US20040033235A1
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Best Local Similarity 100...
Best Local Similarity 100...
36; Conservative
                                                                                    US-10-252-136-3
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LENGTH: 36
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TITLE OF INVENTION: Combination Method For Treating Viral Infections
FILE REPERENCE: INO1358
CURRENT APPLICATION NUMBER: US/10/168,295
CURRENT FILING DATE: 2002-06-19
PRIOR PILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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APPLICANT: BRIDON, Dominique P.
APPLICANT: BUDDELLAB, Niesab
APPLICANT: ROBITAILLE, Martin
APPLICANT: MILNER, Peter G.
TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
FILLE DE INVENTION: INFECTION
FILE REFERENCE: 500862001501/REDC-1512
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                                                                                                                                                                                                                                                                                                                                                           Score 198; DB 4;
Pred. No. 6.6e-16;
; Mismatches 0;
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100.0%; Score 198; DB 5;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
CURRENT APPLICATION NUMBER: US/10/671,282
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,439
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIAN VERSION 3.2
SEQ ID NO 38
LENGTH: 36
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CURRENT FILING DATE: 2004-09-24
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PRIOR APPLICATION NUMBER: US 09/623,533
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/US00/13651
PRIOR FILING DATE: 2000-05-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-168-295-3
; Sequence 3; Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pi
Matches 36; Conservative 0;
                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-38
                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial
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TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
TITLE OF INVENTION: their use in therapy
FILE REPERENCE: TRM-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICAT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT HILING DATE: 2003-09-16
PRIOR PRIOR PILING DATE: 2002-09-27
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100.0%; Pred. No. 6.6e-16;
iive 0; Mismatches 0;
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                                                                       APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUIZ A.
NAME: RACISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                             <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/10671282 Publication No. US20040122214A1 GENERAL INFORMATION:
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Publication No. US20040063637A1
GENERAL INFORMATION:
  FILING DATE: 08-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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SOFTWARE: Patentin version 3.2
SEQ ID NO 38
LENGTH: 36
                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 36, Conservative
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ORGANISM: Artificial
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US-10-671-282-38
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US-10-663-589-38
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APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRED STORMER: US/10/351,641
FILE REFERENCE: 7872-100
CURRENT PEPLICATION NUMBER: US/30,641
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
PRIOR PLICATION NUMBER: 09/082,279
PRIOR PLICATION NUMBER: 09/082,279
PRIOR PLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active

TITLE OF INVENTION: Negions of HIV Envelope Proteins

TITLE OF INVENTION: Negions of HIV Envelope Proteins

FILE REFERENCE: 1900.02600U;

CURRENT APPLICATION NUMBER: US/09/809,060

CURRENT APPLICATION NUMBER: US 60/189,981

PRIOR FILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.0

SEQ ID NO 22
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; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.4%; Score 187; DB 4;
94.4%; Pred. No. 1.3e-14;
tive 1; Mismatches 1;
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93.4%; Score 185; DB 3;
Best Local Similarity 91.7%; Pred. No. 2.2e-14;
Matches 33; Conservative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Core polypeptide US-10-351-641-1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 34; Conservative
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US-09-779-451-47
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APPLICANT: Holmes, Darren L.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION COMPONENTS
FILE REPERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 1909-09-10
PRIOR FILING DATE: 1909-09-10
PRIOR FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-11-066-697-1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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100.0%; Pred. No. 6.6e-16;
iive 0; Mismatches 0;
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100.0%; Pred. No. 6.6e-16;
iive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: US 60/153,406
PRIOR PLILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 545
SOFURMARE: Patentin Ver. 2.1
LENGTH: 36
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Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1051, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100. Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 36; Conservative
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US-11-066-697-1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-10-351-641-1051
                                                                                                                                                                                                                                                                                                                                                                                 US-10-950-010-3
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Search completed: March 6, 2006, 15:50:31
Job time : 94 secs
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Method for Detecting Viral Inactivating Agents
                                                                                                                                                                                                                                                                                                                                                       Score 185; DB 3; Length 36; Pred. No. 2.2e-14; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.4%; Score 185; DB 4; Length 36; 94.4%; Pred. No. 2.2e-14; 1.1ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YTSEIYTLIEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                  ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-01-24

PRIOR APPLICATION NUMBER: 09/350,641

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

SOFTWARE: PROSE DATE: 1999-05-20

SOFTWARE: PROSE DATE: 1999-05-20

SOFTWARE: PROSE DATE: 1999-05-20

LENGTH: 36
                   CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR PLING DATE: 2000-09-10
PRIOR PLING DATE: 2000-02-10
SOFTWARE: PALENT NOS: 77
SOFTWARE: PALENT VEFSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 856, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Core polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 47, Application US/10685801; Publication No. US20040132011A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                       Query Match 93.4%;
Best Local Similarity 91.7%;
Matches 33; Conservative
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FILE REFERENCE: 1900.0300003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 94.4
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guthrie, K.
Merutka, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                           US-09-779-451-47
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US-10-685-801-47
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                                                                                                                                                                                                                                                        Length 36;
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                                                                                                                                                                                                                                                                                                                                         1 YTWIIYTLLEESQNQOEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                    Score 185; DB 4;
Pred. No. 2.2e-14;
2; Mismatches 1.
               CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: US 60/418,341
PRIOR FILING DATE: 2002-10-16
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.2
SEQ ID NO 47
LENGTH: 36
TYPE: PRT
CORGANISM: Human Immunodeficiency virus 1
US-10-685-801-47
CURRENT APPLICATION NUMBER: US/10/685,801
                                                                                                                                                                                                                                                    Query Match 93.4%;
Best Local Similarity 91.7%;
Matches 33; Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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OM protein - protein search, using sw model

March Run on:

6, 2006, 15:37:45 ; Search time 18.3333 Seconds (without alignments) 188.935 Million cell updates/sec

US-09-809-060A-2

Perfect score: Title:

1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

11837

seq length: 0 seq length: 50 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	~	homeofic protein H	hypothetical prote		zinc-binding prote	hypothetical prote		hemoglobin AII - t	renin-2 - mouse (f	troponin T 4f - ra	hemoglobin BII - t	hypothetical prote	ribosomal protein	heat shock protein	hypothetical prote	44	hypothetical prote	androgen-binding p	T3f, fas	probable NADPH-fer	Na+/K+-exchanging	high light-inducib	hypothetical prote		gene 60 protein -	hypothetical prote	arylacetyl-CoA N-a	myosin regulatory
SUMMARIES	. OI	D83682	S27169	B30474	D89972	F86472	502031	T14888	T48342	501808	177411	146523	S01814	F85646	S39857	A34461	A82186	166797	T07291	A40703	S74261	T06541	I54059	T06923	A95135	C82233	831005	G84063	S27170	A34594
	DB	~	~	~	~	~	~	~	~	~	7	7	~	7	7	N	N	~	~	~	~	~	~	0	7	7	7	~	N	~
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d	Query Match	21.2	20.7	19.7	e,	19.7	19.2	٥.	ъ.	В.	18.2	8	89	œ.	17.9	7.	17.7	•	•	17.7	17.7	17.7	17.2	17.2	16.9	16.9	16.9	16.9	16.7	16.7
	Score	42	41	39	39	39	38	38	37	36	36	36	36	36	35.5	32	35	35	32	35	32	32	34	34	ω.	щ.	33.5	Э.	33	33
	Result No.	-	7	m	4	9	9	7	∞.	o	10	11	12	13	14		16	11	18	19	20	21	22	23	24		56			

thymosin beta-11 -	hypothetical prote	somatoliberin - bo	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	androgen-binding p	hypothetical prote	hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote	troponin T, fast s	early protein gp5
S21282	H83653	RHBOS	AG3362	B83894	A95010	C95173	A37405	E64036	H70152	C95128	T13295	T07503	E95248	C34327	EABP59
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43	43	44	49	43	46	46	49	29	30	39	42	43	44	44	45
16.7	16.7	16.7	16.7	16.4	16.4	16.4	16.4	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2
33	33	33	33	32.5	32.5	32.5	32.5	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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RjTakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Mucleic Acids Res. 28, 4317-4317, 2000
Nucleic Acids Res. 28, 4317-4317, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9KG53; UNIPARC:UP10000139521; GB:AP001507; GB:BA000004; NID A;Experimental source: strain C-125 C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: BH0260
                                C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C.Accession: D83682
hypothetical protein BH0260 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <STO>
                                                                                                                                                                                                                                                                                                                                                                          A; Accession: D83682
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Сарв ö Query Match 21.2%; Score 42; DB 2; Length 36; Best Local Similarity 47.6%; Pred. No. 1.1e+02; Matches 10; Conservative 3; Mismatches 8; Indels

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8 LLEESQNQQEKNEQELLELDK 28 |: || || || |: || :| LVNESWEQQRKKIQQLLSDEK 24

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draikyl-CoA N-acyltransferase (EC 2.3.1.-) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Bate: 19-Mar-1997 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: S27169
R;Kelley, M.; Vessey, D.A.
Biochem. J. 288, 315-317, 1992
A;Title: Structural comparison between the mitochondrial aralkyl-CoA and arylacetyl-CoA A;Reference number: S27169; MUID:93075097; PMID:1445276

A,Molecule type: protein A,Residues: 1-41 «KEL» A,Cross-references: UNIPROT:Q9T2U9; UNIPARC:UPI00008C6A3 A,Experimental Bource: kidney C,Keywords: acyltransferase

Gape ö Length 41; Score 41; DB 2; Length 41; Pred. No. 1.8e+02; 3; Mismatches 6; Indels n 20.7%; Similarity 47.1%; 8; Conservative Query Match Best Local Similarity Matches 8; Conserva

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17 1 YTNTIYTLLEBSQNQQE

23 YTNTYHVYSEDLKNGQE 39

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A; Reference number: Z18249; MUID: 98298059; PMID: 9632606
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Pred. No. 4.2e+02;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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C;Superfamily: probable membrane protein ylaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-43 <BRA>
A;Cross-references: UNIPARC:UP10000176609
C;Superfamily: prothymosin alpha
C;Keywords: zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 EESQNQQEKNEQELLELD
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Matches 7; Conservative
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A;Residues: 1-50 <STO>
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            A;Accession: F86472
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S02031
                                                                                                                                                                                                                                                 A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UP100017A32E
A;Note: the authors translated the codon TCC for residue 3 as Pro, CAG for residue 42 as
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;11-46/Domain: homeobox homology (fragment) <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F86472

S. K. Mypothetical protein T3269.50 - Arabidopsis thaliana

C. Species Arabidopsis thaliana (mouse-ear cress)

C. Species 02-Mar-2001

S. Mypothetical protein T3269.50 - Arabidopsis thaliana

C. Data: 02-Mar-2001

C. Accession: F86472

S. Mypothetical Data: Data: C. J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820; 2000

Nature 408, 816-820; 2000

Nature 408, 816-820; 2000

Nature 408, 116-820; 2000

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Cispecies: Staphylococus aureus
Cispecies: Order 10-May-2001
Cispecies: Order 10-May-2001
Cispecies: Order 1: Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
Cispecies: Order 1: Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
Cispecies: Order 1: Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.;
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: UNIPROT:Q99T25; UNIPARC:UPI0000DD7729; GB:BA000018; PID:g13701646;
                            NATIONAL MATERIA MARCOLIC PROTEIN ONDER 8-1
C'Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C'Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C'Accession: B30474
R'Choi, C.L.; Hudson, P.; Stauder, A.; Pietersz, G.; Brandon, M.
R'Choi, C.L.; Hudson, P.; Stauder, A.; Pietersz, G.; Brandon, M.
A'Title: Molecular cloning and characterization of ovine homeo-box-containing genes.
A'Reference number: JT0273; MUID:88255866; PMID:2898416
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A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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19.7%; Score 39; DB 2; Length 46;
Best Local Similarity 34.6%; Pred. No. 3.5e+02;
Matches 9; Conservative 7; Mismatches 10; Indele
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homeotic protein Hox 1.3 homolog - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NTIYTLLEESQNQQEKNEQELLELDK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: || | ::: ||||:|
|NSNYTGGEPKRSRTAYTROQVLELEK 27
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Matches 7; Conserv
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A, Molecule type: DNA
A, Residues: 1-46 < CHO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: D89972
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A;Cross-references: UNIPROT:Q9C6E9; UNIPARC:UPI00000A80F1; GB:AE005172; NID:g11386311; P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1999 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: S02031
R;Brand, I.A.; Heinickel, A.; Kratzin, H.; Soeling, H.D.
Rur. J. Blochen. 177, 561-568, 1981
A;Fitle: Properties of a 19-kDa Zn(2+)-binding protein and sequence of the Zn(2+)-binding A;Reference number: S02031; MUID:89064809; PMID:3197718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Baccession: T14888
R;Wong, K.K.; McClelland, M.; Stillwell, L.C.; Sisk, E.C.; Thurston, S.J.; Saffer, J.D.
Infect. Immun. 66, 3365-3371, 1998
A;Fitle: Identification and sequence analysis of a 27-kilobase chromosomal fragment conta
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A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Est, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; WUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2; Length 50;
Pred. No. 3.8e+02;
3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zinc-binding protein - rat (tentative sequence) (fragment)
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Gapa

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R.Briggs, M.M.; Lin, J.J.; Schachat, F.H.
J. Muscle Res. Cell. Motil. 8, 1-12, 1987
A, Filtle: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle tropor A,Reference number: 146522; MUID:87251333; PMID:2439538
A,Accession: 146523
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: UNIPARC:UP1000016C510; EMBL:U04978; NID:9440816; PIDN:AAA16031.1; PII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
A;Reference number: S01807; MUID:89076216; PMID:3202832
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                           Species: Oryctolagus cuniculus (domestic rabbit)
;Date: 14-Peb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
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C;Species: Lamellibrachia sp.
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-May-2004
C;Accession: S01814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.2%; Score 36; DB 2; Length 32;
46.2%; Pred. No. 5.2e+02;
tive 5; Mismatches 2; Indels
                                                                 Length 30;
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A;Molecule type: mRNA
A;Residues: 1-32 <BRI>
                                                                 DB 2;
                                                                                                                          0; Mismatches
                                                                 Score 36;
Pred. No. '
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C, Keywords: oxygen carrier
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                                                                 18.2%;
                                                                                                                                                                                                                                                                                                                                                                                 roponin T 4f - rabbit (fragment)
                                Query Match
Best Local Similarity 71...,
--has 5; Conservative
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11 EEAQEEEEVHEEE 23
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Best Local Similarity
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                                                                                                                                                                               29 WASLWIW 35
                                                                                                                                                                                                                                     9 WALLWIW 15
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Matches 6; Conserv
        C; Superfamily: Pepsin
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: 177411
R;Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W. Mol. Cell. Biol. 4, 2221-2331, 1984
A;Fitle: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analys A;Reference number: 157576; MUID:85085936; PMID:6392850
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iochem. J. 255, 541-545, 1988
Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
Reference number: S01807; MUID:89076216; PMID:3202832
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                                                                                                                                                                                                                                                                                             W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De
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                                                                                                                                                                            hypothetical protein F15A17.240 - Arabidopsis thaliana Cippothetical protein F15A17.240 - Arabidopsis thaliana (mouse-ear cress)
C;paces 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48342
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clcewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Lamellibrachia sp. (fragment)
Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.7%; Score 37; DB 2; Length 41; 37.5%; Pred. No. 5.2e+02;
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C;Keywords: oxygen carrier
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EDRREMQLM----WANVWS 22
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22 TILEGGETEEDNQEQE 37
||| ::| |::| | TNTFFSLSEQADQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 37.5-
Best G, Conservative
                                                                                                                                                                                                                                                                                                                                                                              Reference number: Z24491; Accession: T48342
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Best Local Similarity
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A, Residues: 1-30 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
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A; Note: F15A17.240
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6, 2006, 15:44:15

C; Accession: A34461

preliminary

A; Accession: F85646

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Ribes-Miller, S.P.; Anderson, C.W.
J. Biol. Chem. 264, 17275-17280, 1989
A;Title: The human double-stranded DNA-activated protein kinase phosphorylates the 90-kDt A;Reference number: A34461; MUID:90008887; PMID:2507541
A;Reterson: A34461
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-30 cLEE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
    17.7%; Score 35; DB 2; Length 30;
Best Local Similarity 43.8%; Pred. No. 6.4e+02;
Matches 7; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP10000177D3F
C;Superfamily: heat shock protein 90
C;Keywords: phosphoprotein
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Job time: 20.3333 secs
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A; Residues: 1-49 <JDA
A; Residues: 1-49 <JDA
A; Residues: 1-49 <JDA
A; Cross-references: UNIPROT: Q06798; UNIPARC: UPIO00005FE0F; EMBL: D13303; NID: g285624; PID
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; ChA
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallech, J.; Harbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Derk, S.; Liu, H.; Mauda, S.; Maucel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sekiguchi, J.; Sekowska, A.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Tognoni, A.; Tosato, V.; Vohiyama,
T.; Minters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasuwoto, K.; Yata, K.; Yata, K.; Yama, K.;
A; Hulters, Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Paterica mumbar, as eguence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Bacillus subfilis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S39657, A69698; S40069
R;Jeong, S.M.; Yoshikawa, H.; Takahashi, H.
Mol. Microbiol. 10, 133-142, 1993
A;Title: Isolation and characterization of the secE homologue gene of Bacillus subtilis.
A;Reference number: S39856; MUID:95058172; PMID:7968510
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A,Experimental source: strain 168
                                                                                                                                       A;Cross-references: UNIPROT:Q8X465; UNIPARC:UP100000D0E36; GB:AE005174; NID:g12514378; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Genetics: A;Genet
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heat shock protein 90 alyha - rabbit (fragment)
C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 23-Feb-1997
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C;Superfamily: Bscherichia coli ribosomal protein L33
C;Keywords: protein biosynthesis; ribosome
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Pred. No. 9.7e+02;
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27.3%;
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Best Local Similarity
Matches 10; Consery
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Best Local Similarity
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                                                                                                   A; Residues: 1-48 <STO>
                                               A; Molecule type: DNA
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OM protein - protein search, using sw model

March Run on:

6, 2006, 15:31:26 ; Search time 114.667 Seconds (without alignments) 137.945 Million cell updates/sec

US-09-809-060A-2

198 1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2443163 segs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

1130394

Minimum DB seq length: 0 Maximum DB seq length: 50

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A_Geneseq_21:* Database

geneseqp2003bs:* geneseqp2003ав:* geneseqp1980s: * geneseqp2000s:* geneseqp2001s:* geneseqp2002s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:* geneseqp2005s:*

SUMMARIES Reg

	ion	Core poly		Vin	Core	Core poly	HIV	Viral cor	Viral DP1	Viral DP1	DP178-lik	DP178-lik	HIV gp41	Hybrid po	Hybrid		Peptide #		HIV-1 tra	DP-178 ho	DP185 cor	DP-178-li	Core poly	HIV-1 qp4	;
	Description	Aav89837	Aab54786	. Aab92245	Aab78238	Aab78237	Aau70180	Abb02830	Abb01245	Abb01244	Aau13791	Aau13790	Aao18772	Ade02850	Ade02716	Abo10164	Adn06923	Ads87258	Ady71493	Aar67698	Aar98399	Aaw17012	Aay89836	Aaq67040	,
SUMMARIES	ID	AAY89837	AAB54786	AAB92245	AAB78238	AAB78237	AAU70180	ABB02830	ABB01245	ABB01244	AAU13791	AAU13790	AA018772	ADE02850	ADE02716	ABO10164	ADN06923	ADS87258	ADY71493	AAR67698	AAR98399	AAW17012	AAY89836	AAG67040	
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de	Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.5	97.5	97.5	97.5	97.5	
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	Ade02349 Hybrid po Adn46689 C-helical Ady2999 HIV-1 gro Aab14573 HIV-1 160 Aag63900 Amino aci
AAY89665 AAB78066 ABB02524 ABB01073 AAU13619 ADE02544 ADE02554 AAY89446 AAY89446 AAY894467 AAY894467 AAY70678 AAB77847 AAB00854 ABB00854 AAU13400	ADE02349 ADN46089 ADY29992 AAB14573 AAG63900
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ALIGNMENTS

AAY89837 standard; peptide; 36 AA. 23-MAY-2000 (first entry) AAY89837; RESULT 1 AAY89837

Core polypeptide fragment T No. 1406.

Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; anglogenic factor.

Unidentified

WO9959615-A1.

25-NOV-1999.

99WO-US011219. 20-MAY-1999;

98US-00082279 20-MAY-1998;

(TRIM-) TRIMERIS INC.

Lambert DM; Anwer MK, Merutka G, Barney S, Guthrie KI,

WPI; 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence.

Disclosure; Page 45; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interlevent, interferon, colony stimulating factor, hormone or anglogenic

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The present invention describes a modified anti-viral peptide (I)

comprising a peptide that exhibits anti-viral activity and a reactive

comprising a peptide that exhibits anti-viral activity and a reactive

group which is reactive with anino groups, hydroxyl groups, or thiol

groups on blood components to form stable covalent bonds. (I) has anti-

coils by inhibiting cell-cell fusion or free virus infection of the level of membrane fusion events between two or more entities, e.g.,

virus-cell or cell-cell, relative to the level of membrane fusion that

cocurs in the absence of the peptide. (I) is useful in the treatment of

patients who are suffering from viral infection, e.g. HIV, RSV, HBIV,

MeV, and SIV. (I) may be administred prophylactically to previously

uninfected individuals. This is useful in cases where an individual has

components of the blood, such as immunosity, serum albumin, red

lived components of the activity is extended for days to weeks.

Chis is due to improved stability in vivo and a reduced susceptibility to
                                                                                                                                                                                            ö
               infection and can be used in anti-viral and anti-fusogenic trearments. Sequences AAY88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides
The peptides of the invention can be used for inhibiting viral
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Long lasting fusion peptide inhibitor; viral infection; antiviral; antifusgenit; mobile blood component; measles virus; MeV; SIV; santian immunodeficiency virus; human parafultuenza virus; HPIV; RSV; human respiratory syncytial virus; human immunodeficiency virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A modified peptide and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds useful for treatment of viral infections, e.g.
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                                                                                                                                                                                            ö
                                                                                                                                                    Length 36;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV antiviral activity exhibiting peptide SEQ ID NO:3.
                                                                                                                                                    100.0%; Score 198; DB 3; 100.0%; Pred. No. 3.4e-17;
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                                                                                                                                                                                                                             1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                      1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF
                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boudjellab N,
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                                                                                                                                                                                                                                                                                                                                                          AAB54786 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                  Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
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                                                                                                               Sequence 36 AA;
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10-SEP-1999;
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05-MAR-2001
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                                                                                                                                                    Query Match
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                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                       RESULT 2
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases the action uptake and interference with physiological processes. AMB90829 to AAB9241 represent peptides which can be used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
peptidase or protease degradation. This minimises the need for more frequent, or even continual, administration of the peptides. AAB54784 tAAB55431 represent peptides used in the exemplification of the present
                                                                                                                                                                    Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thibaudeau K;
                                                        invention. [Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                Length 36;
                                                                                                                                                                  Indels
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                                                                                                                                                                                                      1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                        1 YINTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                              ; Score 198; DB 4;
; Pred. No. 3.4e-17;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Virus related peptide SEQ ID NO:1421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 662; 733pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Milner PG,
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                                                                                                                                                                                                                                                                                                                                AAB92245 standard; peptide; 36
                                                                                                                                100.0%;
100.0%;
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99US-0153406P.
99US-0159783P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2000; 2000WO-US013576.
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                  36; Conservative
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                                                                                                                              Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                            Sequence 36 AA;
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                    AAB92245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and polio virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their
                                                                                                                                                                                                                                                                                                                                                                           enhancer, antiviral; anti-HIV; virucide; hepatotropic; hybrid polypeptide; coiled-coil peptide interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           efficacy and minimises the incidence and severity of adverse side effects. In addition, this increases the sensitivity of the diagnostic
                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                         Core polypeptide, enhancer, antiviral, anti-HIV, virucide, hep antiinflammatory, hybrid polypeptide, coiled-coil peptide inte fusion-related disorder, bacterial infection, viral infection.
Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anwer MK, Lambert DM;
                                        Indels
100.0%; Score 198; DB 4;
100.0%; Pred. No. 3.4e-17;
tive 0; Mismatches 0;
                                                                             1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                     1 YINTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 58; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merutka G,
                                                                                                                                                                                                                 AAB78238 standard; peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00350641.
                                                                                                                                                                                                                                                                                              (first entry)
                  Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                  Core polypeptide T1406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guthrie KI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-147136/15.
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                                                                                                                                                                                                                                                                                              19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2001
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                                                                                                                                                                                                                                                     AAB78238;
  Query Match
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The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibite enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide. The hybrid and core polypeptides can be used for modulation glusgemic events and intracellular processes involving coiled-coil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and spear-egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their effects. In addition, thus increases the sensitivity of adverse side effects.
                                                                                                                                                                                                                                                 Core polypeptide, enhancer, antiviral, anti-HIV, virucide, hepatotropic, antiinflammatory, hybrid polypeptide, coiled-coil peptide interaction; fusion-related disorder; bacterial infection, viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide.
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; Pred. No. 3.4e-17; 
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lambert
1 YINTIYTLLESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YTNTIYTLLEESONQOEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anwer MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 58; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merutka G,
                                                                                                        AAB78237 standard; peptide; 36 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUL-2000; 2000WO-US018772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00350641
                                                                                                                                                                               19-APR-2001 (first entry)
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                                                                                                                                                                                                                Core polypeptide T1405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-147136/15.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                         WO200103723-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1999;
                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                                                                            AAB78237;
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                                                                     RESULT 5
                                                                                         AB7823
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Gaps

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100.0%; Score 198; DB 4; Length 36; 100.0%; Pred. No. 3.4e-17; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 36; Conservative

RESULT 6 AAU70180

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06-AUG-2003 03-JAN-2002

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The invention relates to methods of generating immunogens that elicit neutralising antibodies which target regions of viral envelope proteins such as the gp120/gp1 (gjvcoprotein 120/gjvcoprotein 41) complex of HIV-
1 (human immunodeficiency virus 1). Sequences Adv70179-Adv70198 and
Adv70677-Adv70743 represent stabilising peptides modelling the alpha-
1 (human immunodeficiency virus 1). Sequences Adv70179-Adv70198 and
Adv70677-Adv70743 represent stabilising peptides modelling the alpha-
1 chalical regions of the ectodomain of the HIV-1 transmembrane protein to stabilise fusion-active intermediate structures, which can be used as vaccine immunogens. Immunogens compositions comprise a viral envelope protein or its fragment exterior to the viral membrane, a stabilising peptide to disrupt formation of structural intermediates necessary for viral fusion and entry, and optionally, a viral cell surface receptor or its fragment to form a stabilised, fusion active structure. Antibody binding assays are used to determine the ability of immunogen vaccines to generate an immune response to various forms of ervelope. Virus neutralisation assays can be used to characterise the antibody response raised against HIV-1 gp41 domains. The sequences and methods are useful for inhibiting HIV infection, for inducing an immune very.
                                                                                                                                                                 Human, HIV-1, human immunodeficiency virus; gp41; glycoprotein 41; gp120;
anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
alpha-helical region; ectodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             envelope protein or its fragment exterior to viral membrane, a
stabilizing peptide, and, optionally, viral cell surface receptor or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic composition for inhibiting HIV infection,
                                                                                                                        HIV viral envelope protein stabilising peptide #2.
  AAU70180 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 45; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2001; 2001WO-US008108.
                                                                                                                                                                                                                                                                                                                                                                                                                        L7-MAR-2000; 2000US-0189981P
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PANA-) PANACOS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild CT, Allaway GP;
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                                                                                    14-FEB-2002
                                                                                                                                                                                                                                                      Homo sapiens
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                    Length 36;
                                     Indels
                  100.0%; Score 198; DB 4;
100.0%; Pred. No. 3.4e-17;
tive 0; Mismatches 0;
                                                                       1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                         1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF
                                                                                                                                                                                                       Viral DP178/107-like region peptide T1406.
                                                                                                                           ABB01245 standard; peptide; 36 AA.
                                                                                                                                                                                     (first entry)
                                      Conservative
                                                                                                                                                                   (revised)
                                                                                                                                                                            (revised)
                         Local Similarity
es 36; Conserv
Sequence 36 AA;
                                                                                                                                                                 11-SEP-2003
06-AUG-2003
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                                                                                                                                               ABB01245;
                   Query Match
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                            Best Loca
Matches
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    Length 36;
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Query Match
100.0%; Score 198; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                        1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                               1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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ABB02830 standard; peptide; 36 AA.

11-SEP-2003 (revised)

ABB02830;

RESULT 7
ABB02830
ID ABB0
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AC ABB0
XX
DT 11-S

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(RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-LIAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                              Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus, HIV, respiratory syncytial virus; RSV;
virucide, heptad repeat region, transmembrane protein; gp41; HR1; HR2;
infection.
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                                                        Viral core polypeptide, SEQ ID NO: 1357.
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                                                                                                                                                                                                                                                                                          07-FEB-2001; 2001WO-US003988
                                                                                                                                                                                                                                                                                                                              29-FEB-2000; 2000US-00515965
                    (first entry)
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                                                                                                                                                                                                              WO200164013-A2
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                                                                                                                                                                                              The invention relates to isolated analogues of the heptad repeat region peptides DB178 and DB107. DP178 and DB107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-LIAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region, peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV specification. Updated on 06-MUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                      Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus, HIV; respiratory syncytial virus; RSV; virucide, heptad repeat region; transmembrane protein; gp41; HR1; HR2;
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                                                                                                 Lambert DM, Sista
                                                                                                                                                                                                                                                                                                                                                  th 100.0%; Score 198; DB 4; Length 36; Similarity 100.0%; Pred. No. 3.4e-17; 36; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                      YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viral DP178/107-like region peptide T1405.
                                                                                                 Antczak JB, Delmedico MK, Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                              Disclosure, Page 58; 587pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB01244 standard; peptide; 36
                                      07-FEB-2001; 2001WO-US003988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(revised)
(first entry)
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                                                          29-FEB-2000; 2000US-00515965
                                                                             (TRIM-) TRIMERIS INC
                                                                                                                    WPI; 2001-514829/56
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                  Sequence 36 AA;
WO200164013-A2
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Modified-site
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06-AUG-2003
03-JAN-2002
                  07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection
                                                                                                                                                           infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB01244;
                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                        Matches
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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-555 (heptad repeat region HR1) respectively, of HIV-liA1 transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV september of the sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex.
                                                                                                                                                                                                                                              Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41; antifusogenic; antiviral; HIV transmission; mutant; mutein.
                                                                                                                          Sista P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                          Erickson JB, Lambert DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 198; DB 4;
100.0%; Pred. No. 3.4e-17;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1; isolate LAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP178-like/DP107-like peptide T-1406
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 58; 587pp; English.
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29-FEB-2000; 2000US-00515965.
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                                                                                                                          Delmedico MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 36; Conservative
                                                             (TRIM-) TRIMERIS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200151673-A2.
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                                                                                                                          Antczak JB,
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                                                                                                                                                                                                                                                                                                                  infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU13791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                              amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-555 of gp41 from HIV-LIAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a
                                       The present invention relates to peptides which exhibit anti-retrovir activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41; antifusogenic; antiviral; HIV transmission; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   1 YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                        100.0%; Score 198; DB 4; 100.0%; Pred. No. 3.4e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1; isolate LAI
                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP178-like/DP107-like peptide T-1405
             Disclosure; Page 77; 259pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU13790 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2000; 2000WO-US035727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
es 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442157/47
                                                                                                                                                                                                                                                                                             Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200151673-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU13790;
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Disclosure; Page 77; 259pp; English

DP107/DP178 Acomplex:

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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus I (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-LIAI. The Invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, antivital or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method of treating an HIV infection in an individual, which involves administering in combination a chemokine co-receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its derivative. Other viral infections can also be treated using the method. The present sequence is a peptide derived from HIV and useful in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of HIV infection in an individual involves administration of a combination of chemokine co-receptor five antagonist and a specified HIV envelope polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 198; DB 4;
100.0%; Pred. No. 3.4e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 32; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA018772 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-636513/68.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 AA;
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1 YTNTIYTLLEESQNQOEKNEQELLELDKWASLWNWF 36

ADE02716 standard; peptide; 36 AA.

RESULT 14 ADE0271

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(first entry)

29-JAN-2004

ADE02716;

hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic; pharmacokinetic; fusogenic; insulin; diabetes. Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1223.

'note= "Residue is modified by acetyl group"

Location/Qualifiers

Key Modified-site Modified-site

Unidentified

/note= "C-terminal amide"

99US-00315304. 98US-00082279.

20-MAY-1999;

US6348568-B1 19-FEB-2002

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The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WGSWEGKI or WASLWEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel which polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core.

Thy peptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging structures in vivo. The core polypeptide and hybrid polypeptides are useful for modulating fusogenic events and exhibit antifusogenic or antiviral activity. The novel hybrid polypeptide is useful for decreasing viral infection and modulating intracellular processes involving coiledcoil peptide interactions. The novel hybrid polypeptide is useful for antiorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also or is symptoms of forms of diabetes. The novel hybrid polypeptide is also the core polypeptide is useful for antiorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also events and viral infection that involves cell-cell and/or virus-cell fusion, and for diagnosis and in vivo imaging methods. This sequence the represents an enhancer peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                   Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1357.
                                                                                                                                                                                                                                                                                                                                                                                                            hybrid, enhancer; anti-fusogenic; antiviral; virucide; antidiabetic; pharmacokinetic; fusogenic; insulin; diabetes.
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                                Length 36;
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                                                                       Indels
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                                                                                                                                     YTNTIYTLLESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                          1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                              100.0%; Score 198; DB 5; 100.0%; Pred. No. 3.4e-17;
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                                                                     0; Mismatches
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                                                                                                                                                                                                                                                  ADE02850 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00315304.
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            Query Match
Best Local Similarity 100.u
Local Similarity 100.u
Local 36; Conservative
                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                         ADE02850;
                                                                                                                                                                                                         RESULT 13
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Lambert DM;

Merutka G, Anwer MK,

Guthrie KI,

Barney S,

(TRIM-) TRIMERIS INC.

20-MAY-1998;

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The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WGEWEQKI or WASLWEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel bybrid polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core peptide sequence enhances plarmacokinetic properties of any core copypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging are tructures in vivo. The core polypeptide and hybrid abilypeptides are useful for modulating fusogenic events and exhibit antifusogenic creativity. The novel hybrid polypeptide is useful for decreasing critical infection and modulating intracellular processes involving coiledcoil peptide interactions. The novel hybrid polypeptide comprises insulin or its fragment, so the core polypeptide is useful for ameliorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also call peptide interaction that involves cell and/or virus-cell and viral infection that involves cell-cell and/or virus-cell tusion, and for diagnosis and in vivo imaging methods. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 1223; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-424396/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36 AA;
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1 YTHTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36

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Gaps

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Indels

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100.0%; Score 198; DB 5; 100.0%; Pred. No. 3.4e-17; ive 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 36; Conservative

Length 36;

Query Match 100.0%; Score 198; DB 5; Best Local Similarity 100.0%; Pred. No. 3.4e-17; Matches 36; Conservative 0; Mismatches 0;

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Gaps

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Indels

Length 36;

YINTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36

6, 2006, 15:37:19

Search completed: March Job time : 117.667 secs

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HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
Epstein-Barr virus infection; heptad repeat motif.
1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                           Human immunodeficiency virus 1; isolate SF2.
                                                                                                                                                                                                     Petteway SR;
                                                                          HIV1-SF2 gp41 protein, DP85 peptide.
                               ABO10164 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                       Example, Fig 1, 716pp; English.
                                                                                                                                                              93US-00073028.
94US-00255208.
94US-00360107.
                                                                                                                                                 95US-00485546.
                                                                (first entry)
                                                                                                                                                                                                    Lambert DM,
                                                         (revised)
                                                                                                                                                                                       (TRIM-) TRIMERIS INC.
                                                                                                                                                                                                                 WPI; 2003-465599/44
                                                                                                                        US6518013-B1
                                                                                                                                                 07-JUN-1995;
                                                                                                                                                              07-JUN-1993;
                                                                                                                                                                     07-JUN-1994;
                                                        23-OCT-2003
19~AUG-2003
                                                                                                                                                                           20-DEC-1994;
                                                                                                                                     11-FEB-2003
                                                                                                                                                                                                    Barney SO,
                                            ABO10164;
                                                                                                                                                                                                                                          protein.
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                                                                                                                                                                                                                                                                                 The invention relates to inhibiting (M) transmission of an Epstein-Barr virus to a cell, comprising contacting the cell with an effective concentration of a peptide consisting of a region of 16-39 consecutive amino acids of an Epstein-Barr virus potein for an effective period of time, where the region is recognised by one or more of AliMoTI5, 107x1784 or PLZIP sequence search motifs, the peptide further comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic group, amido group, hydrophobic group, or macromolecular carrier group, and acaboxy is maind group, and is inhibited. The peptides were described the virus to the cell is inhibited. The peptides were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identified by analysing the structure/motifs present in the HIV-1 glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat motif containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic organisms and HIV isolates, looking for DP107/178 structural analogues. The method is useful for inhibiting transmission of Epstein-Barr virus to a cell and Epstein-Barr virus infection. The present sequence is a control peptide used in the study of the DP178 stucture. (Updated on 23-OCT-2003 to standardise OS field)
Inhibiting transmission of Epstein-Barr virus to a cell, by contacting the cell with a peptide consisting of a region of Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 36; Conservative 0; Mismatches 0;
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YIMTIYTLESSONQOEKNEGELLELDKWASLWNWF 36

1 YTNTIYTLLEESQNOOEKNEQELLELDKWASLWNWF 36

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

March 6, 2006, 15:31:50 ; Search time 116.667 Seconds
(without alignments)
217.706 Million cell updates/sec Run on:

US-09-809-060A-2

Title: Perfect score:

1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

90886 Total number of hits satisfying chosen parameters: 2166443 seqs, 705528306 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	immun	nasutiterme	bacteriopha	odium	campylobact	tetraodon n	ndiba	vibrio para	lus ha	dictyosteli	mus musculu	spora
	otion	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	nasut	bacte	plasmodium	campy	tetrac	plasmodium	vibri	bacillus	dicty	ໝາຍໝ	neurospora
	Description	069910	06990	069895	968690	906690	069898	069899	069907	069908	069905	006690	069903	069893	Q69894	Q69904	069901	069902	069891	Q69892	069897	9wxx60	Q9mc62	Q4z1c4	Q4hnw1	Q4t4h4	04yjt6	Q87jd4	Q9kg53	Q55br3	Q675b2	Q789i2
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-	A .	06991	0690	06989	06989	06690	06989	06989	06690	0690	0690	0690	06690	06989	06989	0690	0690	06690	06989	06989	06989	O9XX	O9MC6	Q4 Z1C	Q4HNV	Q4T4F	Q4YJJ	Q87JI	X260	Q55BF	0675E	07891
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* Ouery	Match	93.4	91.9	89.4	89.4	88.4	87.9	87.4	86.9	86.9	86.4	84.8	84.3	83.8	83.8	82.3	79.8	79.8	78.3	76.3	73.2	24.7	24.7	24.2	23.2	23.2	21.7	21.7	21.2	21.2	21.0	20.7
	Score	185	182	177	177	175	174	173	172	172	171	168	167	166	166	163	158	158	155	151	145	49	49	48	46	46	43	43	42	42	41.5	41
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Gp41 (Fragment).
Name-env;
Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.

Last sequence update) Last annotation update)

49 AA.

PRT; Created)

Q69909 9HIV1 PRELIMINARY; Q69909; 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,

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96 2 0905J7 9HIV1 99 2 05XCPI_STRP6 11 2 09T2U9 BOVIN 17 2 04MNY6_BACCE 17 2 0818G2_BACCA 17 2 0811AB_BACCA 17 2 0811AB_BACCA 17 2 0811AB_BACCA 18 2 09GTJ0_PLAPE 18 2 09GTJ0_PLAPE 18 2 09GTJ0_PLAPE 18 2 09GTJ0_PLAPE 18 2 09GTJ0_PLAPE 19 2 09GTJ0_PLAPE 10 2 09SXD6_CAREL 11 2 096ZB3_ARATH	9 2 Q4R7WI_MACFA
33.3 34.3 35.3 36.5 39.5 39.5 39.5 40.5 40.5 40.5 40.5 40.5 40.5 40.5	45 4

ALIGNMENTS

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Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
VCBI_TaxID=11676;
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A CONLEY A.J., Kessler J.A., Boots b.J., Tung J.S., Arnold B.A.,
CONLEY A.J., Kessler J.A., Emots b.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.,
T. "Neutralization of divergent human immunodeficiency virus type 1
T. "Neutralization of divergent human immunodeficiency virus type 1
T. "Neutralization of divergent human immunodeficiency virus type 1
T. "Neutralization of divergent human immunodeficiency virus type 1
T. "Neutral and primary isolates by IAM-41-2F5, an anti-gp41 human
T. "Neutral antibody", U.S.A. 91:3348-3352(1994).
T. EMBL; UG6736; AAA19149:1; -; mRNA.
T. "ROG; GO:0016021; C:integral to membrane; IEA.
R. GO; GO:0016021; C:integral to membrane; IEA.
R. GO; GO:0016031; C:viral envelope; IEA.
R. GO; GO:0016031; C:viral envelope; IEA.
R. InterPro; IPR001328; Env_GP41.
R. Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94211861; PubMed=7512731; Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A., Keller P.M., Shaw A.R., Emint E.A.; "Neutralization of divergent human immunodeficiency virus type 1 variants and primary isolates by IAM-41-2F5, an anti-gp41 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 49 AA; 6167 MW; 0277C4815B8D26FE CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994). BENBL; U06726; AA19139.1; -; mRNA. 91872; 1180. 30; GO-00726; AA19139.1; -; MRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 177; DB 2;
Pred. No. 2.2e-13;
0; Mismatches 3;
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                                             49 AA
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                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,
                           Q69896_9HIV1 PRELIMINARY;
Q69896;
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Q69906_9HIV1 PRELIMINARY;
Q69906;
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                       MEDLINE=94211861; PubMed=7512731;
A Conley A.J., Keseler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Conley A.J., Keseler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Celler P.M., Shaw A.R., Emini E.A.;
T. "Neutralization of divergent human immunodeficiency virus type 1
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T. "Neutralization of divergent human immunodeficiency virus type 1
T. "Neutralization of divergent human immunodeficiency virus type 1
T. "Neutralization of divergent human immunodeficiency virus type 1
T. "Neutralization of divergent human immunodeficiency libed immunoclonal antibody."; mRNA.
T. "RSP, P31872; 1LB0.
T. "RSP, P31872; 1LB0.
T. "RSP, P31872; 1LB0.
T. "RSP, P31872; 1LB0.
T. "RSP, P31872; ILB0.
T. "RSP, P318
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Pred. No. 5.7e-14;
1; Mismatches 2; Indels
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Pred. No. 2.2e-13;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 AA; 6196 MW; E9B618825B832D1E CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IRP000328; Env_GP41.
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Last sequence update)
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EMBL; U06725; AAA19138.1; -; mRNA.
HSSP; P31872; 1LB0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 91.7%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.9%;
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01-NOV-1996 (TrEMBLrel. 01,
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1 Similarity 91.7%;
33; Conservative
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                                                              SEQUENCE
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NCBI_TaxID=11676;
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                                                              NUCLEOTIDE
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Matches

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49 AA; 6214 MW; 29C4ESA8CBD63DD8 CRC64;

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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Conley A.J., Keseler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.J.,
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
                                                                                                                                                                                                                                                                                                                          Length 50;
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EMBL; U06729; AAA19142.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019199; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
NON_TER
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SO
SEQÜENCE 50 AA; 6287 MW; EABA093F0877DBSB CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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Pred. No. 8.5e-13;
4; Mismatches 2;
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EMBL; U06737; AAA19150.1; -; mRNA.
HSSP; Q87973; 2SIV.
                                                                                                                                                                                                                                                                                                             Score 173; DB 2;
Pred. No. 6.6e-13;
2; Mismatches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                       87.4%;
86.1%;
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83.3%;
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069908,
01-NOV-1996 (TEMBLEEL 01,
01-NOV-1996 (TEMBLEEL 01,
01-JUN-2003 (TEMBLEEL 24,
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.10,
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ID Q69907 9HIV1 PRELIMINARY;
AC Q69907;
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hes 30; Conservative
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Lentivirus, Primate lentivirus group.
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MEDLINE=94211861; PubMed=7512731;
Colley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type l
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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                             Score 175; DB 2; Length 49;
Pred. No. 3.8e-13;
3; Mismatches 2; Indels
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86.1%; Pred. No. 5.1e-13;
Live 2; Mismatches 3; Indels
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Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).

EMBL. U06728; AAA19141.1; ", mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005238; F:serructural molecule activity; IEA.

Pfam; PF00517; GP41; 1.
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                 14 YISLIYTLIEESQTQOEKNEKELLELDKWASLWWF 49
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                                    88.4%;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Q69899;
                                                                                                  31; Conservative
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                                                                    Local Similarity
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Q69900_9HIV1 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
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                                                                               MEDLINE-9421186; PubMed=7512731;
Conley A.J., Kessler U.A., Boots L.J., Tung J.S., Arnold B.A.,
Conley A.J., Kessler U.A., Boots L.J., Tung J.S., Arnold B.A.,
Reller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
"Neutralization of divergent hu
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NUCLEOTIDE SEQUENCE.

NUCLEOTIDE 94211861; PubMed=7512731;

Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,

Keller P.M., Shaw A.R., Emini E.A.;

"Neutralization of divergent human immunodeficiency virus type 1

variants and primary isolates by IAM-41-2F5, an anti-gp41 human

monoclonal antibody.";
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Pred. No. 8.5e-13;
4; Mismatches 2; Indels
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34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005199; F:gructural molecule activity; IEA.
PFO0517; GP41; 1.
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Last annotation update)
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EMBL; U06735; AAA19148.1; -; mRNA.
HSSP; P31872; 1LBO.
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Matches 30; Conservative
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NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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NCBI_TaxID=11676;
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MEDLINE=94211861; PubMed=7512731;
Conley A.J.; Kessler J.A.; Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.L., Emini E.A.,
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL; U06733; AAA19146.1; "RRNA.
                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.,
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
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EMBL; U06730; AAA19143.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001931; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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                                                             Last sequence update)
Last annotation update)
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005199; F:structural molecule activity;
Interpro; IRR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
NON TER
1 34 34
SEQUENCE 34 AA; 4226 MW; E609273F6164BDB0 CR(
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83.3%; Pred. No. 2.6e-12;
live 2; Mismatches 4
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                                        Created)
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                                   01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,
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EMBL; U06724; AAA19137.1; -; mRNA
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Q69904_9HIV1
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
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Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
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MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.N.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2FS, an anti-gp41 human
antibody.";
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    ch 84.3%; Score 167; DB 2; Length 34; 1 Similarity 93.8%; Pred. No. 2.2e-12; 30; Conservative 2; Mismatches 0; Indels
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PP00517; GP41; 1.
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Last sequence update)
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994)
EMBL; U06723; AAA19136.1; -; mRNA.
HSSP; P31872; 1LBO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QG9893 9HIV1 PRELIMINARY;
Q69893
01-NOV-1996 (TEMBLEEL: 01,
01-NOV-1996 (TEMBLEEL: 01,
01-JUN-2003 (TEMBLEEL: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q69894 9HIVI PRELIMINARY;
Q69894;
Query Match
Best Local Similarity
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069893 9H1
069893 9H1
07089893 9H2
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                     Gape
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Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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GO; GO: 0016021; C:integral to membrane; IEA.

GO; GO: 0019031; C:virtal envelope; IEA.

GO; GO: 0015198; F:structural molecule activity; IEA.

InterPro; IPR000328; Env GP41.

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NON TER 34 34

SEQÜENCE 34 AA; 4182 MW; A37CAA60A164AEF0 CRC64;
                                                                                                                                                                             34 34 34
34 AA; 4182 MW; A37CAA60A164AEF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0001919; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41:
Pfam; PP00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994)
EMBL; U06734; AAA19147.1; -; mRNA.
HSSP; P31872; 1LB0.
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82.3%; Score 163; DB 2;
Best Local Similarity 90.6%; Pred. No. 6.5e-12;
Matches 29; Conservative 2; Mismatches 1
                                                                                                                                                                                                                                               Score 166; DB 2;
Pred. No. 2.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                  3 IYTLLEESQVQQEKNEQELLELDKWASLWNWF 34
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Job time : 118.667 secs
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                                                                                                                                                                                                                                                  Query Match 83.8%;
Best Local Similarity 96.9%;
Matches 31; Conservative
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069904;
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Sequence 1357, Ap
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Sequence 1543, Ap
                                                                                                                 (without alignments)
107.578 Million cell updates/sec
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Sequence 14
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                                                                                               March 6, 2006, 15:43:35.; Search time 27.6667 Seconds
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF
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S-08-405-551A-3
S-08-471-913A-3
S-08-685-264A-3
S-09-082-279B-1357
S-08-474-349A-3
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5-09-834-744-1357

5-09-515-965A-1357

5-09-350-641C-1357

5-08-481A-1357

5-08-481A-1357

5-08-481A-1357

5-08-481A-1421
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5-08-255-208A-3
5-08-973-952-3
5-08-470-896-3
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                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                572060 segs, 82675679 residues
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Maximum Match 100%
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                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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                                                                                                                                                                                Perfect score:
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	sequence 642, App
US-09-082-279B-1051 US-09-315-304B-1051 US-09-834-784-1051 US-09-350-641C-1051 US-09-350-841A-1051 US-09-350-841A-1051 US-09-315-304B-856 US-09-315-304B-856 US-09-779-451-47 US-09-350-641C-856 US-09-350-841A-856 US-09-350-841A-856 US-09-350-841A-856 US-09-350-841A-856 US-09-350-841A-856 US-09-350-841A-856 US-09-350-841C-856 US-09-350-841A-856 US-09-350-841A-856 US-09-350-841A-856 US-09-350-841A-856 US-09-350-350-841A-856 US-09-350-350-841A-856 US-09-350-350-841A-856 US-09-350-341A-856 US-09-350-341A-856	US-09-834-784-642
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ALIGNMENTS

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RESULT 1

US 08-486-099-3

US 08-486-099-3

SEQUENCE 3. Application US/08486099

Fatent No. 6013263

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Bolognesi, Dani P.
APPLICANT: Bolognesi, Dani P.
APPLICANT: Bolognesi, Dani P.
APPLICANT: Langloid, Call T.
APPLICANT: Langloid, Alphones J.
TITLE OF INVENTION: COMPOSITIONS POR INHIBITION OF
TITLE OF INVENTION: REMEANE FUSION-ASSOCIATED EVENTS, INCLUDING HERAITIES
TITLE OF INVENTION: BURGANE DESS.
APPLICANT: Langloid, Alphones J.
TITLE OF INVENTION: BURGANE DESS.
ADDRESSEE: Pennie & Edmonds
CITY: New York
CUUTRY: New York
CUUTRY: New York
CUUTRY: New York
CUUTRY: PLOSOF AND AND ADDRESSEE: Pennie & Edmonds
CITY: New York
CUNTRY: PLOSOF ADDRESS:
COMPUTER REAL DESSEE: Pennie William #1.30
CUNTRY: PLOSOF ADDRESS:
CURRENT APPLICATION NAM:
CURRENT APPLICATION NAM:
RECISTRATION NUMBER: 30,742
RECISTRATION NUMBER: 30,743
RECISTRATIO
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Length 36;

100.0%; Score 198; DB 2;

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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTA A
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                    E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08475668A Patent No. 6060065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 787:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10036-2711
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                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wid, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambort, Dennis M.
APPLICANT: Lambort, Dennis M.
APPLICANT: Trice OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: TRANSMISSION
VUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennis & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FURGIS

COMPUTER: IBM PC compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: BATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223B

FILING DATE: 07-7010-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: COTAZI, LAURA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (212) 869-9741/8864

TELEERAX: (212) 869-9741/8864

TELEERAX: GALP PERNIE
        Pred. No. 3.3e-17; 
; Mismatches 0;
                                                                     YTNTIYTLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                            1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 198; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YTNTIYTLLEESONOOEKNEQELLELDKWASLWNWF 36
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100.0%; Pred. w..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                  Sequence 3, Application US/08484223B Patent No. 6020459
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Patent No. 6654265
GENERAL INFORMATION: 4
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
      Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                 US-08-484-223B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-919-597-3
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APPLICANT: Barney, Shawn O.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Compositions R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphones J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 198; DB 2;
100.0%; Pred. No. 3.3e-17;
tive 0; Mismatches 0;
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Gaps

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APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TWAISON-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 36;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DETERMINE Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-UM-1995
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTTAIL, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 198; DB 2; Best Local Similarity 100.0%; Pred. No. 3.3e-17; Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YINTIYTLEESONOOEKNEOELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08471913A Patent No. 6093794
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 790-9090
(212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 3:
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
                                 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 36 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
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                                                                                                                                                                 TYPE: amino STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                              US-08-485-551A-3
   TELEFAX:
TELEX: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-471-913A-3
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FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: COLUZI, LUMRA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 198; DB 2;
100.0%; Pred. No. 3.3e-17;
iive 0; Mismatches 0;
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1155 Avenue of the Americas
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Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
VENTION: METHODS FOR II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08485551A
Patent No. 6068973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matthews, Thomas J. Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELERAX: (212) 869-9741/86
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 790-9090
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                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: BAlognes
APPLICANT: Matthews
APPLICANT: Matthews
APPLICANT: Barney, S
APPLICANT: Lambert,
APPLICANT: Lambert,
APPLICANT: Lambert,
APPLICANT: Lambert,
APPLICANT: Lambort,
APPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-475-668A-3
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; OTHER INFORMATION: Core polypeptide US-09-082-279B-1357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08474349A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER:STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 36 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: USA
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US-08-474-349A-3
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                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matchews, Stawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: US/08/485,264A
FILING DATE: US/JUN-1995
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: COCULZI, LAURE 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELEPRAK: (212) 790-9090
TELEFRAK: (212) 869-9741/8864
TELERY: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                        YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennie & Edmonds LLP
55 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1357, Application US/09082279B
Patent No. 6258782
                                                                                                                                          Sequence 3, Application US/08485264A Patent No. 6228983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guthrie, Kelly
Mærutka, Gene
Anwer, Mohmed
Lambert, Dennis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barney, Shawn
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CITY: New York
STATE: New York
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APPLICANT: Barney, S
APPLICANT: Guthrie,
APPLICANT: Mærut%a,
APPLICANT: Anwer, Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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US-09-082-279B-1357
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STREET: 11
                                                                                                  RESULT 7
US-08-485-264A-3
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APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphones J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TURNS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennis & Edmonds
STREET: 1155 Avenue of the Americas
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TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES FILE OF INVENTION: PHARMACOKINETIC PROPERTIES CURRENT APPLICATION NUMBER: US/09/082,279B CURRENT FILING DATE: 1998-05-20 NUMBER OF SEQ ID NOS: 1515 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1357 LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A FILING DATE: 07-JUN-1995 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COTLAZI, LAURA A.
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 198; DB 2; Best Local Similarity 100.0%; Pred. No. 3.3e-17; Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YTNTIYTLLESQNQQEKNEQELLELDKWASLWNWF 36
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07-JUN-1994
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                             amino acid
                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                      US-08-255-208A-3
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APPLICANT:
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US-08-470-896-3
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                                            Gaps
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APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
PRIOR FILICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
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Length 36;
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Lambert, Dennis M.
Petteway Jr., Stephen R.
VENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
ROWINON: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                    YTNTIYTLLEESONOOEKNEOELLELDKWASLWNWF 36
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100.0%; Score 198; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0;
                                                                               1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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100.0%; Score 198; DB 2; 100.0%; Pred. No. 3.3e-17;
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1667
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 1357
LENGTH: 36
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                                                                                                                                                                                                                Sequence 1357, Application US/09315304B Patent No. 6348568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Core polypeptide US-09-315-304B-1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennie & Edmonds LLP
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Patent No. 6440656
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Matthews, Thomas J
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bolognesi,
APPLICANT: Wild, Cwel,
APPLICANT: Wild, Cwel,
APPLICANT: Lambert, DAPPLICANT: Petteway JAPPLICANT: PETEWAY JAPPLICANT: PETEWAY JAPPLICANT: PETEWAY JAPPLICANT: TITLE OF INVENTION: T
                                                                                                                                                                                                                                                                                                Guthrie, K.
Merutka, G.
                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
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STREET: 11
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                                      36;
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  Query Match
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APPLICANT:
                                      Matches
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GENERAL INFORMATION:
APPLICANT: Johnson, M. Ross
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNOBEFICIENCY VIRUS AND OTHER VIRAL INFECTIC
TITLE OF INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 7872-036
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Score 198; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                   ; Score 198; DB 2;
; Pred. No. 3.3e-17;
0; Mismatches 0;
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ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08973952A Patent No. 6475491
                 NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REPRENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMISSION
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Matthews, Thomas J
                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100....
Thes 36; Conservative
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 36
                                                                                                                                                                                                                                          36 amino acids
                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
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NAME: COLUZZÍ, LGULA A.
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 7872-028
TELECOMUNICATION INFORMATION:
TELEFAX: (212) 790-9990
TELEFAX: (212) 869-9741/8864
TELEK: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Core polypeptide US-09-834-784-1357
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ORGANISM: Artificial Sequence
     07-JUN-1995
                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
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Job time: 28.6667 secs
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APPLICANT: Matchews, Thomas J.
APPLICANT: Matchews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphons J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
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                                                                                                                                                      CCUNTRY: USA

ZIP: 10036-271

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
OFFICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
GIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTAZZI, LAUKA A.
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/IOCKET NUMBER: 30,742
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100.0%; Pred. No. 3.3e-17;
iive 0; Mismatches 0;
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08485546A Patent No. 6518013 GENERAL INFORMATION:
NUMBER OF SEQUENCES: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-896-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS:
                                                                                                                             New York
: USA
                                                                                                  New York
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US-08-485-546A-3
                                                                                                                                                   COUNTRY:
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       Length 36;
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100.0%; Score 198; DB 2;
100.0%; Pred. No. 3.3e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                             1 YINTIYILLEESQNQOEKNEQELLEIDKWASLWNWF 36
                                                                                                                                                                                                                                                                                 1 YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF 36
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein March Run on:

6, 2006, 15:31:26; Search time 114.667 Seconds (without alignments) 137.945 Million cell updates/sec

US-09-809-060A-3 200 1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

113,0394 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 50 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:*geneseqp2003bs:*geneseqp2004s:* geneseqp1990s:* geneseqp1980s:* geneseqp2000s:* geneseqp20028: geneseqp2001s; A_Geneseq_21 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:

SUMMARIES

		de			SOFTHERIES		
Result No.	Score	Query	Query Match Length	DB	ID	Description	
	200	100.0	36	. 2	AAR67699	Aar67699 DP-178 ho	
8	200	100.0	36	N	AAR98400	Aar98400 Peptide c	
m	200	100.0	36	~	AAW17013		
4	200	100.0	36	4	AAB54787	Aab54787 HIV antiv	
S	200	100.0	36	4	AAB92246	Aab92246 Virus rel	
y	200	100.0	36	4	AAB7823.9	Aab78239 Core poly	
7	200	100.0	36	4	AAB78240	Aab78240 Core poly	
a 0	200	100.0	36	4	AAU70181	Aau70181 HIV viral	
σ	200	100.0	36	4	ABB02832		
10	200	100.0	36	4	ABB02831	Abb02831 Viral cor	
11	200	100.0	m	4	AAG67041	HIV-1	
12	200	100.0	36	4	ABB01246	Abb01246 Viral bP1	
13	200	100.0	ĕ	4	ABB01247	Abb01247 Viral DP1	
14	200	100.0	36	4	AAU13793		
15	200	100.0	ň	4	AAU13792	Aau13792 DP178-lik	
16	200	100.0	36	4	AAU14013	Aau14013 DP178 hom	
17	200	100.0	36	2	AA018773	Aao18773 HIV gp41	
18	200	100.0	36	Ŋ	ADE02851	Ade02851 Hybrid po	
19	200	100.0	36	Ŋ	ADE02852	Ade02852 Hybrid po	
20	200	100.0	36	9	AB010165	Abol0165 HIV1-RF g	
21	200	100.0	36	8	ADN06924	Adn06924 Peptide #	
22	200	100.0	36	æ	ADS87259	Ads87259 HIV-1 gp4	
23	200	100.0	36	σ	ADY71494	Ady71494 HIV-1 tra	
24	185	92.5	48	œ	ADU80528	Adu80528 Transmemb	

	ABEYBA399 DF185 COF ABW17012 DP-178-11 ABG67040 HTV-1 GD4			Adu80508 Transmemb Adu80513 Transmemb	Transm HIV-1	Adz40271 HIV-1 gp4 Adz40285 HIV-1 gp4	Adu80507 Transmemb Adz40265 HIV-1 gp4	Core	Aab77633 Core poly Abb02115 Viral cor
ADZ40286 AAR67698	AAK98399 AAW17012 AAG67040	AAU14012 AAY22914	ABG68385 ABU57792	ADU80508 ADU80513	ADU80527 ADZ40266	ADZ40271 ADZ40285	ADU80507 ADZ40265	AAY89838 AAY89839	AAB77633 ABB02115
	36 22			48 48 8			48 48 9		
92.5	987.0	92.0	91.0	91.0 91.0	91.0 91.0	91.0	90.5 90.5	90.2 90.2	90.06
185	184 184	184	182 182	182	182 182	182 182	181 181	180.5	180
5 5 7 7 8 7 8	28 6	330	33	34 35	36 37	3 8 9 6	4 4 1	4 4 4 3	4. 4. 4. 7.

ALIGNMENTS

RESULT 1

antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI; human immunodeficiency virus; transmembrane protein; gp41; alpha helix; DP-178 homologue derived from HIV-1 RF has antiviral activity. AAR67699 standard; peptide; 36 AA. (first entry) (revised) (revised) leucine zipper; DP-185 16-OCT-2003 25-MAR-2003 24-AUG-1995 AAR67699; AAR67699

Human immunodeficiency virus; (RF isolate). WO9428920-A1.

22-DEC-1994.

94WO-US005739 07-JUN-1994; 93US-00073028 07-JUN-1993;

(UYDU-) UNIV DUKE.

Lambert DM; Barney SO, Matthews TJ, Wild CT, Bolognesi DP, Petteway SR;

WPI; 1995-036105/05.

Computer search generated synthetic peptides - are inhibitors of HIV transmission.

Example, Fig 1; 182pp; English

This peptide is isolated from HIV-1 isolate RF, and is a homologue of the peptide DP-178. DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalant protein-protein interactions, and possess anti-viral activity. The peptide inhibits transmission to uninfected cells, and can also be used as type and/or subtype specific diagnostic tools. (Updated on 25-MAR-2003 to correct PN

41;

RESULT 2 AAR98400

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AAW17012-W17016 are DP-178 homologues that are useful in the treatment of HIV infection. DP-178 is a peptide corresponding to residues 638-673 of HIV type 1 glycoprotein 41 (gp41) transmembrane protein. DP-178 and its derivatives/homologues are used in combination with a therapeutic agent, e.g a reverse transcriptase, viral protease, cytckine, glycosylation or viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides work by inhibiting viral replication or inhibiting transmission. They may also be used in vaccines for protecting against HIV infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compsns. contg. DP-178 or DP-107 in combination with other therapeutic agent - useful for treatment of HIV infection, esp. by inhibiting replication or transmission of HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Long lasting fusion peptide inhibitor; viral infection; antiviral; antifusogenic; mobile blood component; measles virus; MeV; SIV; simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV; human respiratory syncytial virus; human immunodeficiency virus; HIV.
                                                                                                                                                                                                      HIV; SIV: human; simian immunodeficiency virus; glycoprotein 41
transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;
                                                                                                                                                                 DP-178-like peptide useful for treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV antiviral activity exhibiting peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YTGIIYNLLESSQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Pred. No. 1.4e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                       Human immunodeficiency virus 1; RF isolate.
                        AAW17013 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB54787 standard; peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00481957
                                                                                                                                                                                                                                                 replication; transmission.
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(first entry)
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1es 36; Conservative
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                                                                                                           (revised)
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                                                                                                                                                                                                                                                                                                                              WO9640191-A1
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01-JUL-1997
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05-MAR-2001
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Matches
    RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an isolated peptide recognised by an ALLMOTIS, 107x178x4 or PLZIP sequence search motif.
                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antifusogenic activity, antiviral capability, coiled-coil peptide, ALLMOTIS, 107x178x4, PLZIP search motif, viral transmission, HIV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lambert DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.
                                                                                  Length 36,
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field.) (Updated on 16-OCT-2003 to standardise OS field)
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100.0%; Pred. No. 1.4e-17;
tive 0; Mismatches 0;
                                                                              Query Match 100.0%; Score 200; DB 2; Best Local Similarity 100.0%; Pred. No. 1.4e-17; Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        influenza virus; hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 1, 471pp, English.
                                                                                                                                                                                                                                                                                                   AAR98400 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
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Petteway SR, Langlois AJ;
                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
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                                       Sequence 36 AA;
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17-FEB-1997
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Gaps

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Indels

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Best Loca Matches

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Length 36;

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The present invention describes a modified anti-viral peptide (I) comprising a peptide that exhibits anti-viral activity and a reactive comprising a peptide that exhibits anti-viral activity and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds. (I) has anti-viral and anti-fusogenic activities. (I) inhibits viral infection of cells by inhibiting cell-cell fusion or free virus infection or to reduce the level of membrane fusion events between two or more entities, e.g., virus-cell or cell-cell, relative to the level of membrane fusion that occurs in the absence of the peptide. (I) is useful in the treatment of patients who are suffering from viral infection, e.g. HIV, RSV, HPIV, MeV, and SIV. (I) may be administered prophylactically to previously uninfected individuals. This is useful in cases where an individual has been subjected to a high risk of exposure to a virus. By bonding of longlycen components of the blood, such as immunoplobin, serum albumin, red blood cells and platelets the activity is extended for days to weeks. This is due to improved stability in vivo and a reduced susceptibility to peptidase or protease degradation. This minimises the need for more frequent, or even continual, administration of the peptides. AAB54794 to AAB5431 represent peptides used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise Of field)
                                                                                                                                                                                                                                                                                                                                                                                                             A modified peptide and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds useful for treatment of viral infections, e.g.
                                                                                                                                                                                                                                                                                                              Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 173-174; 211pp; English.
Human immunodeficiency virus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human immunodeficiency virus.
                                                                                                                                         17-MAY-2000; 2000WO-US013651
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                                                                                                                                                                                                                                                               (CONJ-) CONJUCHEM INC.
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                                               WO200069902-A1.
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10-SEP-1999;
                                                                                            3-NOV-2000
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Length 36; Indels 100.0%; Score 200; DB 4; 100.0%; Pred. No. 1.4e-17; iive 0; Mismatches 0; 1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36 1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36 Query Match Best Local Similarity 100. 8

AAB92246 standard; peptide; 36

(first entry) 22-JUN-2001

Virus related peptide SEQ ID NO:1422

Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl, thiol; hormone, growth factor, neurotransmitter.

Homo sapiens Synthetic

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comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (III) and a relative group (II) (e.g. succinimidyl and maleimido groups) attached to bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and appecificity as bonding to large molecules decreases
                                                                                                                                                                                                                                                                                                           Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a modified therapeutic peptide (I)
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                                                                                                                                                                                                                                 Thibaudeau K;
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Pred. No. 1.4e-17;
0; Mismatches 0;
                                                                                                                                                                                                                                 Milner PG, Holmes DL,
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                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 662-663; 733pp; English
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                                                                                                                99US-0134406P.
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                                                                        17-MAY-2000; 2000WO-US013576
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Best Local Similarity luv...
...hes 36; Conservative
                                                                                                                                                                                                                                 Bridon DP, Ezrin AM,
                                                                                                                                                                                           (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                       WPI; 2001-112059/12.
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WO200069900-A2
                                                                                                                17-MAY-1999;
                                                                                                                                                    15-OCT-1999;
                                    23-NOV-2000.
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RESULT 6 AAB78239

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AAB78239 standard; peptide; 36 AA. 19-APR-2001 (first entry) AAB78239;

Core polypeptide T1407.

Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic; antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.

Unidentified.

WO200103723-A1.

18-JAN-2001

10-JUL-2000; 2000WO-US018772

09-JUL-1999;

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Best Local Similarity 100.
Matches 36, Conservative
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                          (TRIM-) TRIMERIS INC.
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                                                                                                                                                                                                                                                      polypeptide.
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                                                                                  Barney S,
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AAB 78240
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polypepture exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptides can be used for modulating fusions: other uses include preventing, treating coiled agnoshing disconserved by the coiled peptide interactions. Other uses include preventing, treating and/or call peptide interactions of the uses include preventing, treating and/or neurotransmitter exchange and sperm-egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus. cespiratory syncytial virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and creduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side effects. In addition, this increases the sensitivity of the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, HIV-1; human immunodeficiency virus; 9041; 9lycoprotein 41; 9p120
anti-HIV; stabilising peptide; viral envelope protein; 9lycoprotein 120;
alpha-helical region; ectodomain.
                       New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core
                                                                                                                                                                          The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV viral envelope protein stabilising peptide #3.
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100.0%; Pred. No. 1.4e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YTGIIXNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                        Disclosure; Page 58; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU70181 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         procedure in which they are used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild CT, Allaway GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36 AA;
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                                                                         polypeptide.
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                                                                                                                                                                                                                                                                                                               The present sequence is a core polypeptide which may be linked to an polypeptide captide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the modulating fusogenic events and intracellular processes involving coiledcoil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of diagnosing that exchange and sperm-egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus, respiratory syncytial infections caused by human immunodeficiency virus, respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus, Epstein-Barr Virus, hepatitis B virus, Mason-Ffizer virus and pollo virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence everity of adverse side effects. In addition, this increases the sensitivity of the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic; antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.
                                                                                                                                                               New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                    Lambert
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100.0%; Pred. No. 1.4e-17;
iive 0; Mismatches 0;
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                                                                    Anwer MK,
                                                                                                                                                                                                                                                                     Disclosure; Page 58; 151pp; English.
                                                                    Merutka G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB78240 standard; peptide; 36 AA
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                                                                 Guthrie KI,
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Gaps

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Length 36; Indels Immunogenic composition for inhibiting HIV infection, comprises viral envelope protein or its fragment exterior to viral membrane, a stabilizing peptide, and, optionally, viral cell surface receptor or its

WPI; 2001-626098/72.

fragment

Lambert DM;

Merutka G, Anwer MK,

99US-00350641

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                                         neutralising antibodies which target regions of viral envelope proteins such as the gpl20/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-
1 (human immunodeficiency virus 1). Sequences Auv70179-Auv70198 and
Auv70677-AAUv7043 represent stabilising peptides modelling the alpha-
helical regions of the ectodomain of the HIV-1 transmembrane protein to
stabilise fusion-active intermediate structures, which can be used as
vaccine immunogens. Immunogens expressions comprise a viral envelope
protein or its fragment exterior to the viral membrane, a stabilising
peptide to disrupt formation of structural intermediates necessary for
viral fusion and entry, and optionally, a viral cell surface receptor or
its fragment. The stabilising peptide is capable of associating with the
structure. Antibody binding assays are used to determine the ability of
immunogen vaccines to generate an immune response to various forms of
envelope. Virus neutralisation assays can be used to characterise the
antibody response raised against HIV-1 gp41 domains. The sequences and
methods are useful for inhibiting HIV infection, for inducing an immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
                               The invention relates to methods of generating immunogens that elicit
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100.0%; Pred. No. 1.4e-17;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTGIIXNELEESQNQQEKARQELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                   response in an animal and for raising antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viral core polypeptide, SEQ ID NO: 1359.
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 Page 45; 84pp; English
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(revised)
(first entry)
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Best Local Similarity 100.
Matches 36; Conservative
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06-AUG-2003
03-JAN-2002
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ABB02832
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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-

Disclosure; Page 525; 587pp; English.

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respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as R8V and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-633 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-LIAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV specification. The present sequence is a peptide provided in the specification. (Updated on 06-NUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
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                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 200; DB 4; Best Local Similarity 100.0%; Pred. No. 1.4e-17; Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viral core polypeptide, SEQ ID NO: 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB02831 standard; peptide; 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(revised)
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                                                                                                                                                                                                                                            Sequence 36 AA;
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06-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB02831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB02831
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Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; 9p41; HR1; HR2;

infection.

Viruses.

Viral DP178/107-like region peptide T1407.

(first entry)

03-JAN-2002 11-SEP-2003 06-AUG-2003

(revised) revised)

ABB01246 standard; peptide; 36 AA.

ABB01246;

/note= "N-terminal is substituted by Ac"

Location/Qualifiers

Modified-site

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-LIAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as R8V and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (R8V) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus, HIV; respiratory syncytial virus; RSV;
virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
infection; DP185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sista P;
                                  Length 36;
                                                                Indels
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                                                                ö
                                                                                                             YTGIIYNLLEESQNQQERORGQELLELDKWANLWNWF 36
                               100.0%; Score 200; DB 4; 100.0%; Pred. No. 1.4e-17;
                                                                                            1 YTGIIYNLLEESQNQQEXNEQELLELDKWANLWNWF 36
                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                      HIV-1 gp41 peptide DP178 homologue DP-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erickson JB,
                                                                                                                                                                                                       AAG67041 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example, Fig 1, 587pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2001; 2001WO-US003988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-FEB-2000; 2000US-00515965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MK,
                                                                                                                                                                                                                                                                       (revised)
(first entry)
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Best Local Similarity 100.
Matches 36. Conservative
                                                             36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514829/56.
                          Query Match
Best Local Similarity
Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200164013-A2
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03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection.
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                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTGIIYNLLESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 200; DB 4;
100.0%; Pred. No. 1.4e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                   /note≈ "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 58; 587pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB01247 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2001; 2001WO-US003988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                           07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antczak JB,
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ID ABB(
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Gaps

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Indels

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100.0%; Score 200; DB 4; 100.0%; Pred. No. 1.4e-17; ive 0; Mismatches 0;

YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36

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RESULT 12 ABB01246

YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36

Length 36;

06-AUG-2003 03-JAN-2002

(TRIM-) TRIMERIS INC

Antczak JB,

WO200164013-A2

Viruses

07-SEP-2001

WPI, 2001-514829/56.

infection

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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus i (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-LIAI. The invention also relates to a method of identifying compounds that inhibit the formation of a disrupts a DP107/DP178 complex, both in the presence of a test compound, in a reaction mixture containing DP107 and absence of a test compound; which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention
                                                                                                                                                                                                                                                                                              107/DP178 complex, especially compounds with antifusogenic, antiviral intracellular modulatory activity, by detecting the formation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
                                                                                                                                                                                                                                                                    Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antivi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
                                                                                                                                                                                  Merutka G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antifusogenic; antiviral; HIV transmission; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 200; DB 4;
; Pred. No. 1.4e-17;
0; Mismatches 0;
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                                                                                                                                                                                  Lawless MK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DP178-like/DP107-like peptide T-1407
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 77; 259pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                  Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU13792 standard; peptide; 36 AA
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100.0%;
                                              05-JUL-2000; 2000WO-US035727
                                                                                         99US-00350841
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Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                                                                                Lackey JW,
                                                                                                                                     (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                            WPI; 2001-442157/47
                                                                                                                                                                                                                                                                                                                                        DP107/DP178 complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 AA;
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Modified-site
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                                                                                      19-JUL-1999;
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                                                                                                                                                                                  Jeffs P,
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AAU13792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection. The present sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                           Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41; antifusogenic; antiviral; HIV transmission; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 100.0%; Score 200; DB 4; Local Similarity 100.0%; Pred. No. 1.4e-17; les 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1; isolate LAI
                                                               Viral DP178/107-like region peptide T1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DP178-like/DP107-like peptide T-1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 58; 587pp; English.
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                                                                                                                                                                                                                                                                                                                                          07-FEB-2001; 2001WO-US003988
                                                                                                                                                                                                                                                                                                                                                                                     29-FEB-2000; 2000US-00515965
(revised)
(first entry);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delmedico MK,
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Sequence 36 AA;

Query Match

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WO200151673-A2

Synthetic.

21-NOV-2001

AAU13793
IID AAU11
IID AAU

AAU13793;

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Gaps

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PF 05-JUL-1999; 99US-00350841.

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PR 09-JUL-1999; 99US-00350841.

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TRIM-) TRIMERIS INC.

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Telentifying a compound that inhibits the formation of or disrupts a per property of the pro
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Query Match 100.0%; Score 200; DB 4; Length 36; Best Local Similarity 100.0%; Pred. No. 1.4e-17; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps

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1 YTGIIYNLLEBSQNQQEKNEQELLELDKWANLWNWF 36

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Search completed: March 6, 2006, 15:37:20 Job time : 115.667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 6, 2006, 15:37:45 ; Search time 18.3333 Seconds
(without alignments)
188.935 Million cell updates/sec

US-09-809-060A-3 200 1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

11837

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
1: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description	៉្ន	hemoglobin AII - t	hemoglobin BII - t	hypothetical prote	5.7K hypothetical	zinc-binding prote	LDH-A - mouse (fra	GUT8-2a protein -	transketolase (EC	troponin T 4f - ra	troponin T 3f - ra	Ω.	ú	high light-inducib	renin-2 - mouse (f	heat shock protein	probable NADPH-fer	R2R3-MYB transcrip	hypothetical prote	photosystem I 9K p	hypothetical prote	hypothetical prote	hypothetical prote	gene 60 protein -	pachytene arrest p	hypothetical prote	homeotic protein H	L33 protein (impor	calreticulin, uter
SUMMARIES	TD	D83682	801808	S01814	D89972	F86472	S02031	I48240	856313	877793	I46523	166797	T48342	S74261	T06923	177411	A34461	T06541	T52125	AG3362	PU0026	B83894	A82186	C97551	831005	S72456	D71345	B30474	o	E33208
	Length DB	36 2		•	50 2							38 2		•	•	•	•	20 2	•								41 2			
di	Query Match Length	21.0	20.5	20.5	19.5	19.5	19.0	18.5	18.5	18.2	18.0	18.0	18.0	18.0		17.5	17.5	17.5	17.2	17.0	17.0	16.8	16.5	16.5	16.5	16.5	16.2	16.2	16.2	16.0
	Score	42	41	41	39	39	38	37	37	36.5	36	36	36	36	36	35	35	35	34.5	34	m		33	33	33	33	32.5	32.5	2	32
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	nypothetical prote hypothetical prote
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	15.
31 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	31
	4 4 5

ALIGNMENTS

RESULT 1 BASSAGE Typochetical protein BH0260 [imported] - Bacillus halodurans (strain C-125) Mypochetical protein BH0260 [imported] - Bacillus halodurans C; Species: Bacillus halodurans Mylate and Experiment and Experime	ne deep- MID:3202 UPI00001	Score 41; DB 2; Length 24; Pred. No. 1e+02;
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Gaps

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Length 50 7; Indels

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <STO>
A;Cross-references: UNIPROT:Q9C6E9; UNIPARC:UPI00000A80F1; GB:AE005172; NID:g11386311; P3
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            zinc-binding protein - rat (tentative sequence) (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: S02031
R;Brand, I.A.; Heinickel, A.; Kratzin, H.; Soeling, H.D.
Bur. J. Blochem. 177, SG1-568, 1989
A;Title: Properties of a 19-kDa 27(2+)-binding protein and sequence of the Zn(2+)-binding A;Reference number: S02031; MUID:89064809; PMID:3197718
                                                                                                                                                                                                           Score 39; DB 2;
Pred. No. 4e+02;
                                                                                                                                                                                                                                                                 3; Mismatches
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C;Species: Nicotiana tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 1-43 <BRA>
A,Crose-references: UNIPARC:UPI0000176609
C;Superfamily: prothymosin alpha
C;Keywords: zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VVEEEENGAEEEEETAE 19
                                                                                                                                                                                                                                                                                                                 10 EESQNQQEKNEQELLELD 27
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                                                                                                                                                                                                           19.5%;
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Best Local Similarity 38.5-
Best Local 7; Conservative
                                                                                                                                                                                                                                                                 8; Conservative
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Best Local Similarity
Matches 8; Conserva
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hes 8; Conserv
A; Accession: F86472
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Matches
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                                                                  hemoglobin BII - tube worm (Lamellibrachia sp.) (fragment)
(species: Lamellibrachia sp.
C;Species: Lamellibrachia sp.
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-May-2004
C;Accession: 80.814
R;Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
A;Reference number: 801807; MUID:89076216; PMID:3202832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vencer, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q99T25; UNIPARC:UPI00000D7729; GB:BA000018; PID:g13701646; A;Experimental source: strain N315
C;Genetics:
A;Gene: SAS053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species Staphylococcus aureus
C;Species Capate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89972
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawäno, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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Pred. No. 2.1e+02;
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Pred. No. 4e+02;
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                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-45 SSUZ>
A;Cross-references: UNIPARC:UP1000017711A
C;Keywords: oxygen carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 QEKNEQELLELDKWANLWN 34
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70.0%;
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Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-50 < KUR>
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A; Status: preliminary
                                                                                                                                                                                                                                                                                    A; Accession: S01814
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rededues: 1-42 <RES>
A;Cross-references: UNIPARC:UPI000016CBFE; EMBL:X03753; NID:g49920; PIDN:CAA27387.1; PID:
C;Superfamily: L-lactate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                region of mouse lactate dehydroge
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 148240
R;Fukasawa, K.M.; Li, S.S.
Biochem, J. 235, 435-439, 1986
A;Title: Nucleotide sequence of the putative regulatory region of mouse lact A;Reference number: 148240; MUID:86295627; PMID:3017306
                                                   Gaps
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  Length 43;
                                                   6; Indels
19.0%; Score 38; DB 2; 38.9%; Pred. No. 4.5e+02;
                                                   5; Mismatches
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Best Loca Matches

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 166797
R;Briggs, M.M.; Schachat, F.
Dev. Biol. 158, 503-509, 1993
A;Title: Origin of fetal troponin T: Developmentally regulated splicing of a new exon in A;Reference number: 153073; MUID:93345743; PMID:8344466
A;Accession: 166797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q62620; UNIPARC:UPI00000E7D00; EMBL:U04981; NID:g440822; PIDP
C;Superfamily: troponin T
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Cibace: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
Cibacession: T48142
Ribevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Cleews, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A;Reference number: 224191
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C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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C;Accession: S74261

W. M.; Marcady, M.; Schmidt, J.M.; Schachat, F.
FEBS Lett. 350, 37-40, 1994

A;Title: Identification of a fetal exon in the human fast Troponin T gene.

A;Reference number: S48660; WUID:94341369; PMID:8062920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9LYW4; UNIPARC:UP100000AA77A; EMBL:AL163002
A;Experimental source: cultivar Columbia; BAC clone F15A17
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-38 <RES>
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19 ILETILEGGETEEDNQEQE 37
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31.6%;
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Best Local Similarity 41.27
Best Local 7; Conservative
                                                       Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-41 <BEV>
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A, Note: F15A17.240
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Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cibate: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
Ciscossion: 146523
Ribriggs, M.M.; Lin, J.J.; Schachat, F.H.
Ribriggs, M.M.; Lin, J.J.; Schachat, F.H.
A; Muscle Res. Cell. Mottil. 8, 1-12, 1987
A; Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle tropc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S77793
R; Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A; Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiolc A; Reference number: S77739; MUID:96059641; PMID:7476192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPROT:049047; UNIPARC:UPI00000B7B19; EMBL:233230; NID:g514477; PID Experimental source: ATCC 27343
Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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                                  R,Taylor, C.B.; Green, P.J.
Plant Mol. Biol. 28, 27-38, 1995
A;Title: Identification and characterization of genes with unstable transcripts (GUTs)
A;Reference number: S56313; MUID:95306789; PMID:7787185
A;Accession: S56313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mycoplasma capricolum
C;Date: 09-Oct_1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: transketolase; thiamin pyrophosphate-binding domain homology
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                                                                                                                                                                                                                                                                                                   Score 37; DB 2; Length 44;
Pred. No. 6e+02;
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N/Alternate names: protein MC315
                                                                                                                                                                                                                                                                                                                                                             17;
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Pred. No. 6.2e+02;
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Pred. No. 5.5e+02;
5; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                5 IYNLLEESQNQQEKNEQELLELDKWANLWNW 35
                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
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                                                                                                                                                                                                                                                         A; Cross-references: UNIPARC: UPI000017B0A6
                                                                                                                                                                                                                                                                                                        18.5%;
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46.2%;
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Best Local Similarity
Matches 6; Conserv
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C,Superfamily: transket
C,Keywords: transferase
                                                                                                                                                                         A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-44 <TAY>
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                          Accession: S56313
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C. Accession: T06233
R. Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
Bubmitted to the EMBL Data Library, July 1995
A. Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A. Reference number: 215840
A. Accession: T06923
A. Statuus: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residues: 1-49 < STI>
A. Cross-references: UNIPROT: P48367; UNIPARC: UP1000013A441; EMBL: U30821; NID: G1016083; PI
A. Experimental source: strain Pringsheim LBSSS
A;Residues: 1-48 <BRI>
A;Cross-references: UNIPROT:P45378; UNIPARC:UPI0000711F8; EMBL:U14644; NID:G557029; PID C;Superfamily: troponin T C;Keywords: alternative splicing; phosphoprotein; skeletal muscle
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C;Species: Mus musculus (house mouse)
C;Species: O2-Mug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: 177411
R;Field, L.U.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W.Mol. Cell. Biol. 4, 2321-2331, 1984
A;Fiele: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analysh;Reference number: 157576; MUID:85085936; PMID:6392850
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C;Superfamily: Pepsin
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T06923
T106923
C;Species: cyanelle protein homolog - Cyanophora paradoxa cyanelle
C;Species: cyanelle Cyanophora paradoxa
C;Dete: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: C6923
R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant
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Pred. No. 8.7e+02;
4; Mismatches 6; Indels
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A;Genome: cysnelle
C;Superfamily: high light-inducible protein ss12542
C;Keywords: cyanelle
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A;Molecule type: DNA
A;Residues: 1-30 <RES>
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Job time : 19.3333 secs
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13 YEEEEEAQEEEEVOEEE 29
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Best Local Similarity 41.2%;
Matches 7; Conservative
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2166443 seqs, 705528306 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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Match Length
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Perfect score:
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Q905e1 human immun Q905e9 human immun Q905il human immun Q816q9 gossppium h Q816q8 gossppium h Q816q9 gossppium h Q65bx3 dictyosteli Q816q7 gossppium h Q675bx mus musculu Q66ky9 speleonecte Q5xpl streptococc Q9tws6 lamellibrac Q4mmy6 bacillus ce Q730n7 bacillus ce Q818g2 bacillus ce	date) dae, Orthoretrovirinae, S., Arnold B.A., iency virus type 1 in anti-gp41 human i, IEA.	Length 50; Indels 0; Gaps 0; ite) ite)
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42 21.0 36 42 21.0 36 42 21.0 45 42 21.0 45 42 21.0 45 41.5 20.8 30 41.5 20.8 50 41 20.5 39 41 20.5 47 41 20.5 47 41 20.5 47	1 9HIV1 66998_9HIV1 PRELIMINAR 66998_6 HIV1 PRELIMINAR 1-NOV-1996 (TrEMBLrel. 1-NOV-1996 (TrEMBLrel.) p41 (Fragment). name=nnv, name=nnv, name=nnv, name=nnv, name=nnv, name=nnv, name=nnv, name=nnv, nonlogalinarelen EDLINE=94211861, PubMe DOLINE=94211861, PubMe DOLINE=94211861, PubMe DOLINE=94211861, PubMe DOLINE=94211861, PubMe DOLINE=94211861, PubMe DOLINES SEQUENCE SEQUENCE DOLINE=94211861, PubMe DOLINES SEQUENCE SEQUENCE DOLINES SEQUENCE DOLINES SEQUENCE DOLINES SEQUENCE SEQUENCE DOLINES SEQUENCE OF GO:0016021, C:integ O; GO:0016021, C:integ O; GO:0016021, C:integ O; GO:0016021, C:integ O; GO:0016021, C:integ O; GO:0016021, C:integ O; GO:0019031, C:viral O; GO:0019031, C:vira	y Match Local S hes 34 1 15 2 9HIV1 69900_9H 69900_9H 1-NOV-19 1-NOV-19 1-JUN
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.,
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2FS, an anti-gp41 human
                                                                                                                                                                                                                   MEDILINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini B.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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Pred. No. 1.5e-13;
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                                                                                                                                                                                                                                                                                                                 monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL; U06729; AaA19142.1; -; mRNA.
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterProc. IPROG0328; Entructural molecule activity; IEA.
Frank PF00517; GP41: 1.
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GG; GG:0019031; C:viral envelope; IEA.
GG; GG:0001998; Fstructural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994)
EMBL; U06740; AAA19153.1; -; mRNA.
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Best Local Similarity 88.9
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Q69910;
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01-JUN-2003 (TrEMBLrel.
GP41 (Fragment).
Name=env;
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Best Local Similarity
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Lentivirus; Primate lentivirus group.
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       NUCLEOTIDE SEQUENCE.
MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini B.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
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50 AA; 6300 MW; EABA093F086C79E1 CRC64;
                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL; U06730; AAA19143.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; PR000328; Env GP41.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
NON TER.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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EMBL; U06739; AAA19152.1; -; mRNA.
HSSP; P31872; 1LB0.
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Pred. No. 6.1e-14;
3; Mismatches 1;
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Q69909;
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QG9899 9HIV1 PRELIMINARY;
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RESULT 3
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Matches

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Gaps

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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
 Gaps
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MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
MEDLINE=17. M., Sheller J.A., Emini E.J., Tung J.S., Arnold B.A.,
Keller P.M., Shevi, Emini E.J., Tung J.S., Arnold B.A.,
Keller P.M., Sherin E.J., Emini E.J., Tung J.S., Arnold B.A.,
Meutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL, U06726, AAA19139.1; -; mRNA.
HSSP; P31872; 1LB0.
                                                                                                                                                                                                                        [1]
NUCLECTIDE SEQUENCE.
MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Enfini E.A.,
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
variants and primary isolates of IAM-41-2F5.
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Pred. No. 2.3e-13;
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 Indels
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GG; GG:0019031; C:viral envelope; IEA.
GG; GG:00019198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
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                                                                                                                     Created)
Last sequence update)
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5;
                     1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                 7 YTSLIYTLIBESQNQQEKNEQELLELDKWASLWNWF 42
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EMBL; U06725; AAA19138.1; -; mRNA.
HSSP; P31872; 1LBO.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                  PRT;
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Э.,
                                                                                                                                                                            Human immunodeficiency virus 1.
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88.9%;
                                                                                                                                 (TrEMBLrel. 01, (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q69896, 9HIV1 PRELIMINARY, Q69896; 01-NOV-1996 (TrEMBLrel. 0)
                                                                                                Q69895_9HIV1 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 88.9
nes 32; Conservative
Conservative
                                                                                                                     01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11676;
                                                                                                                                                                                                            NCBI_TaxID=11676;
                                                                                                                                                       Gp41 (Fragment).
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31;
                                                                                                                                 01-NOV-1996
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=env;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                      9HIV1
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Matches
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Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Lentivirus, Primate lentivirus group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini B.A.;
"Neutralization of divergent human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variants and primary isolates by IAM-41-2F5, an anti-gp41 human
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                                                                                                                                                                                                          Length 49;
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                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                             0277C4815B8D26FE CRC64;
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GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IFF0003238; Env_GP41.
Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0019031; C:viral envelope, IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994)
EMBL, U06738; AAA19151.1; -; mRNA.
HSSP, Q87973; 2SIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                          Score 178; DB 2;
Pred. No. 2.3e-13;
                                                                                                                                                                                                                                                                                                                              14 YTGLIYTLLEESQIQQEKNEQELLELDKWASLWNWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 YTSIIYTLLEKSQNQQEKNEKELLELDKWTNLWNWF
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                                                                                                                                                             49 AA; 6167 MW;
                                                                                                                                                                                                                               88.98;
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Conservative
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Q69908;
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Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw KR., Emini E.A.,
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 AA; 6214 MW; 29C4E5A8CBD63DDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P31872; LLBO.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994). EMBL; U06736; AAA19149.1; -; mRNA. 90; 60:001607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.08
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    Q69906_9HIV1 PRELIMINARY;
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Q69891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Les 29; Conserv
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                                                                                                        Gp41 (Fragment).
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SEQUENCE
                                                                                                                           Name=env;
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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                                  MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini B.A.;
"Neutralization of divorgent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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MEDLINE=94211861; PubMed=7512731;
Colley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.K., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 174; DB 2; Length 49;
Pred. No. 6.9e-13;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                          49 49
49 AA; 6241 MW; 29C4E5A8CBC7CDD8 CRC64;
                                                                                                                                                                                          HESP; 087973; 2517.

GO; GO: 0016021; C: integral to membrane; IEA.

GO; GO: 0019031; C: integral to membrane; IEA.

GO; GO: 0019031; C: viral envelope; IEA.

GO; GO: 0015198; FESTURICTURAL molecule activity; IEA.

InterPro; IPR000328; Env_GP41.

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NON_TER 49 49

SEQÜENCE 49 AA; 6241 MW; 29C4E5A8CBC7CDD8 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).

EMBL, 106735, AAA19148.1; -; mRNA.

HSSP, P31872; 1LBO.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

Pfam; PF00517; GP41; 1.
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                                                                                                                                     monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994)
EMBL; U06737; AAA19150.1; -; mRNA.
HSSP; Q87973; 2SIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YTGIIYNLLEESQNQQEKNEQELLELDXWANLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                    87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     069905;
069905;
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Matches 30; Conservative
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Best Local Similarity 88.2°
Matches 30; Conservative
[1]
NUCLEOTIDE SEQUENCE
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                                  ö
   Length 49;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 41 41 41 41 41 41 AA; 5082 MW; 0B9C7E2CDD403CC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA
                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                14 YTSLIYTLIEESQTQQEKNEKELLELDKWASLWNWF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody,",
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL; U06721; AAA19134.1; -; mRNA.
                                                              1 YTGIIYNLLEESQNQOEKNEQELLELDKWANLWNWF 36
Score 169; DB 2;
Pred. No. 2.6e-12;
4; Mismatches 3
                                                                                                                                                                            41 AA.
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                                                                                                                                                                                                         Created)
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Pfam; PF00517; GP41; 1.
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NON_TER
SEQUENCE
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RESULT 11 Q69906_9HIV1

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EMBL; U06724; AAA19137.1; -; mRNA.
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
                                   Gaps
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                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.

MEDILIPE=9421861, PubMed=7512731;

MEDILIPE=9421861, PubMed=7512731;

Conley A.U., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,

Keller P.M., Shaw A.R., Emini E.A.;

"Neutralization of divergent human immunodeficiency virus type 1

variants and primary isolates by IAM-41-2F5, an anti-gp41 human

monoclonal antibody.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini B.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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       Length 41;
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                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
                                                                                                                                                                                                       Last sequence update)
Last annotation.update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 166; DB 2; Len
Pred. No. 3.9e-12;
    84.0%; Score 168; DB 2; L
88.2%; Pred. No. 2.8e-12;
ive 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                               Lonal antibody "; Natl. Acad. Sci. U.S.A. 91:3348-3352(1994). U06723; AAA19136.1; -; mRNA.
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                                                            3 GIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                          1 GIIYNLIETSQNQQERNELELLELDKWASLWNWF 34
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                                                                                                                                                                34 AA
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                                                                                                                                                              PRT;
                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                              Human immunodeficiency virus 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
Query Match
Best Local Similarity 88.2°
Matches 30, Conservative
                                                                                                                                                             Q69893_9HIV1 PRELIMINARY;
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Q69894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00517; GP41; 1
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tes 30; Conserv
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                                                                                                                              RESULT 13
Q69893_9HI
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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                                                                                                                                                                                                                                                                   Gape
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Conley A.J., Keseler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.,;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2FS, an anti-gp41 human
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HSSP; P31872; 1LBO.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral molecule activity; IEA.

InterPro; IPR000328; Env.GP41.

NON TER

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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019198; Fsructural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
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Last annotation update)
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EMBL; U06722; AAA19135.1; -; mRNA.
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85.3%; Pred. No. 8.3e-12;
                                                                                                                                                                                                                      Score 166; DB 2;
Pred. No. 3.9e-12;
                                                                                                                                                                                                                                                                                                                                  3 GIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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88.2%;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9HIV1 PRELIMINARY;
                                                                                                                                                                                                                                           Best Local Similarity 88.2
Matches 30; Conservative
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Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=11676;
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SEQUENCE
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March 6, 2006, 15:43:35 ; Search time 27.6667 Seconds
(without alignments)
107.578 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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200 1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLMNWF 36 572060 segs, 82675679 residues Gapop 10.0 , Gapext 0.5 US-09-809-060A-3 **BLOSUM62** Scoring table: Perfect score: Sequence: Searched:

308952 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2 6/ptcdata/1/iaa/RE_COMB.pep:*
/cgn2 6/ptcdata/1/iaa/RE_COMB.pep:* Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	4	4	4	4	4	4	4	Sequence 4, Appli	4	135	1359,	4, App	13	1359,	4, App	4,	4	4	1358,	1359,	1358,		1358,	1359,	1358,	1359,
SUMMARIES	ID	US-08-073-028-4	US-08-486-099-4	US-08-360-107A-4	US-08-484-223B-4	-08-9	-08-475-6	8	4	-08-554-		9-082-279B-13	-60-	÷	US-09-315-304B-1358	US-09-315-304B-1359	US-08-255-208A-4	US-08-973-952-4	80-	-08-485	-09-834	-09-83	-09-515-965A-1	-09-515	-09-350-641C-1	-09	US-09-350-841A-1358	US-09-350-841A-1359
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dr	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Sequence 4, Appli Sequence 1422, Ap Sequence 1422, Ap Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1543, Appli Sequence 642, App Sequence 642, App	Seguence 3, Appli
US-08-487-266A-4 US-09-623-548A-1422 US-10-252-136-4 US-09-657-276-1422 US-08-488-741-4 US-08-073-028-3 US-08-554-616-3 US-08-554-616-3 US-09-350-841A-1543 US-09-350-841A-1543 US-09-350-6412 US-09-315-364-642 US-09-315-364-642 US-09-315-3634-642 US-09-350-641A-642 US-09-350-641A-642 US-09-350-641A-642 US-09-350-641A-642 US-09-350-641A-642	US-08-484-223B-3
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ALIGNMENTS

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
COURSEPONDENCES: 74
CORRESPONDENCES. 74
ADDRESSEE: Pennie & Edmonds SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: BLICATION NUMBER: US/08/073,028 FILING DATE: 07-JUN-1993 FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION: SSEE: Pennie & Edmonds T: 1155 Avenue of the Americas New York : New York MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 4, Application US/08073028 Patent No. 5464933 (212) 869-8864/9741 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 36 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: unknown MOLECULE TYPE: peptide COMPUTER READABLE FORM: MEDIUM TYPE: Floppy USA 10036 STATE: NE STREET: CITY: No US-08-073-028-4

Gaps ô Length 36; Indels Query Match
100.0%; Score 200; DB 1;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0;

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1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36

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TRANSMISSION
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                                                                                                           ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bolognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T. APPLICANT: Barney, Shawn O. APPLICANT: Lambert, Dennis M.
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TELEY. 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRRACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
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TITLE OF INVENTION: METH
TITLE OF INVENTION: OF M
TITLE OF INVENTION: TRAN
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: USA
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, INFORMATION:
NAME: COTUZZI, INFORMATION:
TELEFONMINICATION INFORMATION:
TELEFOX: (212) 869-9741/8864
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
TENNYMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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4.6e-18;
1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Score 200;
Best Local Similarity 100.0%; Pred. No. 4
Matches 36; Conservative 0; Mismatche
                                                                                                                                                                                                 APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INF
TITLE OF INVENTION: WEMBRANE FUSION-ASSC
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08360107A Patent No. 6017536
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Lambert, Dennis M.
Petteway, Stephen R.
Langlois, 'Alphonse J.
                                                                                                     Sequence 4, Application US/08486099
Patent No. 6013263
                                                                                                                                                                 Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
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Matthews, Thomas J.
Wild, Carl T.
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MOLECULE TYPE: peptide
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: New York
RY: USA
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STRANDEDNESS:
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APPLICANT: Bolognee
APPLICANT: Matthewe
APPLICANT: Mathewe
APPLICANT: Lambert,
APPLICANT: Lambert,
APPLICANT: Lambert,
APPLICANT: Lambert,
APPLICANT: Lambert,
                                                                                                                                            GENERAL INFORMATION:
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                                                            RESULT 2
US-08-486-099-4
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STATE:
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APPLICANT: MILE CARL T.
APPLICANT: MILE CARL T.
APPLICANT: Barney, Shawn O.
APPLICANT: Langlais, Alphones J.
APPLICANT: Langlais, Alphones J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: TANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                            CUMPIXE: 0.036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CCLUZZ, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTGIIYNLLEESQNQQEKNEQELLELDKWANLWWF 36
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100.0%; Pred. No. 4.6e-18;
ive 0; Mismatches 0;
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SEQUENCE CHARACTERISTICS:
LENGTH: 36 amiliary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
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TELEX: 60
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    TELEX:
INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Alphonse J. METHADS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datenful Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/919,597
 Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 200; DB 2; Best Local Similarity 100.0%; Pred. No. 4.6e-18; Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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E: Pennie & Edmonds
1155 Avenue of the Americas
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-UIN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08919597
Patent No. 6054265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petteway, Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bolognesi, Dani P.
Matthews, Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELECOMMUNICATION INFORMATION:
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Barney, Shawn O.
Lambert, Dennis M.
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                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Matchews,
APPLICANT: Wild, Car,
APPLICANT: Barney, SI
APPLICANT: Lambert, I
APPLICANT: Langlois,
APPLICANT: Langlois,
TITLE OF INVENTION: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Langlois,
                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bologr
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                                                                                                                                                                                                                                                                                                            US-08-484-223B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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US-08-919-597-4
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FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS TRANSMISSION
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APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
                                                                                                                                                                          Length 36;
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SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,668A

FILING DATE: 07-2010-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REPRERENCE/DOCKET NUMBER: 7872-026

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    Query Match
100.0%; Score 200; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                       1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Pred. No. 4.6e-18;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS FOR I
TITLE OF INVENTION: FUSION-ASSOCIATED
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08475668A Patent No. 6060065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 790-9090
(212) 869-9741/8864
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Matches 36; Conservative
36 amino acide
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                    TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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Sequence 4, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
BOLOGNESI, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
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Sequence 4, Application US/0848551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Stephen R.
APPLICANT: Lambert, Stephen 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUNTX: New .-.
STATE: New .-.
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCHILIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/485,551A
TLING DATE: 07-JUN-1995
TLING DATE: "ANTION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 100.0%; Score 200; DB 2; 1 Similarity 100.0%; Pred. No. 4.6e-18; 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAULE A.
REGISTRATION NUMBER: 30,742
REFERNICE/DOCKET NUMBER: 7872-023
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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STREET: 1155 Avenue of the Americas

STATE: New York

CONTITY. New York

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ATTOMACHICATION NUMBER: 10.704.11.913A

ADDITIONAL SYSTEM: 10.704.11.913A

ATTOMACHICATION NUMBER: 10.704.11.913A
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                                               Length 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1358
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACCKINETIC PROPERTIES
FILE REFERENCE: 7872-007
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
                                                                                                                                                                     1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Pred. No. 4.6e-18;
ive 0; Mismatches 0;
                                            100.0%; Score 200; DB 2;
100.0%; Pred. No. 4.6e-18;
ive 0; Mismatches 0;
                                                                                                                                      1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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Pred. No. 4.6e-18;
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100.0%; Score 200; D
Best Local Similarity 100.0%; Pred. No. 4.6
Matches 36; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                Sequence 1358, Application US/09082279B Patent No. 6258782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1359, Application US/09082279B
Patent No. 6258782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Core polypeptide US-09-082-279B-1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Core polypeptide US-09-082-2798-1359
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                                            Query Match
Best Local Similarity 100.0
Matches 36; Conservative
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Best Local Similarity 100.
Matches 36; Conservative
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Merutka, Gene
Anwer, Mohmed
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Merutka, Gene
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APPLICANT: Barney,
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SEQ ID NO 1359
LENGTH: 36
    US-08-485-264A-4
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APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Perteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
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                                                                                                                                                                                                                                                                                                                                                                                             Length 36;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLAZI, LUMRA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 200; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                  NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Belogues; Dani P.
APPLICANT: Mathews, Thomas J.
APPLICANT: Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
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                                                                                                                                                                                                                         LENGTH: 36 amino acids
rYPE: amino acid
rYPE: alingle
rYPE: peptide
US-08-554-616-4
ATTORNEY/AGENT INFORMATION
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC TITLE OF INVENTION: PROPERTIES FILE REFERENCE: 782-052 CURRENT APPLICATION NUMBER: US/09/315,304B CURRENT FILING DATE: 1999-05-20 PRIOR FILING DATE: 1999-05-20 PRIOR FILING DATE: 1998-05-20 NUMBER OF SEQ ID NOS: 1667 SOFTWARE: PSESSEQ for Windows Version 3.0 SEQ ID NO 1358 LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 200; DB 2;
100.0%; Pred. No. 4.6e-18;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 36; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                            Sequence 4, Application US/08474349A

Patent No. 6333395
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Stephen R.
APPLICANT: Lambert, Dennis M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
                                            1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Score 200; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0;
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T: 1155 Avenue of the Americas
New York
: New York
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Batent No. 6148568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merytka, G.
APPLICANT: Anwer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMINICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 4:
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; MOLECULE TYPE: peptide
US-08-474-349A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
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STRANDEDNESS:
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                                                                                                                                                                             RESULT 13
US-08-474-349A-4
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STATE: NE
COUNTRY:
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APPLICANT: Barney, S.
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, M.
APPLICANT: Guthrie, M.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
APPLICANT: 1990-05-20
ARION FILING DATE: 1990-05-20
ARION FILING DATE: 1998-05-20
ARION SEQ ID NOS: 1667
ARION LAMBER OF SEQ ID NOS: 1667
ARION LAMBER ARE REARENCE TO Windows Version 3.0
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                                      1 YTGIIYNLLEESQNQQEKNEQELLEELDKWANLWNWF 36
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100.0%; Pred. No. 4.6e-18;
tive 0; Mismatches 0;
1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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; Sequence 1359, Application US/09315304B
; Patent No. 6348568
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Sequence 1358, Ap
Sequence 1359, Ap
Sequence 4, Appli
Sequence 39, Appli
Sequence 39, Appli
Sequence 1422, Appli
Sequence 1422, Appli
Sequence 1422, Appli
Sequence 534, Appli
Sequence 534, Appli
Sequence 534, Appli
Sequence 537, Appli
Sequence 539, Appli
Sequence 3, Appli
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Sequence 1421, Ap
                                                                        March 6, 2006, 15:44:30 ; Search time 94 Seconds
(without alignments)
160.020 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                     US-09-809-060A-3
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1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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US-10-252-136-4
US-10-351-641-1358
US-10-267-682-4
US-10-267-682-4
US-10-267-682-4
US-10-671-282-39
US-10-671-282-39
US-10-68-295-4
US-11-066-697-1422
US-10-950-010-934
US-10-950-010-534
US-10-950-010-537
US-10-950-010-537
US-10-950-010-537
US-10-950-010-537
US-10-350-010-537
US-10-267-682-3
US-10-267-682-3
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US-10-267-682-3
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                                                                                                                                                                                                     1867569 segs, 417829326 residues
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                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                      OM protein
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Sequence 4, Application US/10252136

Sequence 4, Application US/10252136

Publication No. US20030103998A1

GENERAL INFORMATION:
APPLICANT: Johnson, M. Ross
APPLICANT: Johnson, M. Ross
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNOBEFICIENCY VIRUS AND OTHER
TITLE OF INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 7872-036

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: US/08/973,952

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 82

SEQ ID NO 4
      109, App
856, App
856, App
19, App
109, App
101, App
101,
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Sequence 3, Application US/09809060

Publication No. 20020010317A1

SEQUENCE 3. Application US/09809060

Publication No. 120020010317A1

SEQUENCE 3. Application Scalar

SEQUENCE 3. Application Scalar

TITLE OF INVENTION: A Method for Generating Immunogens that Elicit

TITLE OF INVENTION: A Method for Generating Immunogens that Elicit

TITLE OF INVENTION: A Method for Generating Immunogens that Elicit

TITLE OF INVENTION: A Method for Generating Immunogens that Elicit

TITLE OF INVENTION: Regions of HIV Envelope Proteins

FILE REFERENCE: 1900.026001

CURRENT APPLICATION NUMBER: US/09/809,060

CURRENT PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: US 60/189,981

PRIOR APPLICATION NUMBER: US 60/189,981

PRIOR PELING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 87

SEQ ID NO 3

LENGTH: 36
      Sequence
Sequence
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100.0%; Score 200; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0;
US-09-854-816-109
US-10-351-641-856
US-10-950-010-336
US-09-709-050-19
US-09-709-70-1051
US-10-685-801-44
US-10-685-801-44
US-09-709-050-17
US-09-85-801-42
US-09-860-206-42
US-09-860-206-42
US-09-860-206-42
US-09-860-202-10
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; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-3
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Sequence 1359, Application US/10351641

Publication No. US2030186874A1

GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Anwer, M.
APPLICATION NUMBER: 09350,641

PRIOR PILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-06-20
                                                                                                                                                                             Gaps
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APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
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100.0%; Score 200; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                      1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Score 200; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PLING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SEQ ID NO 1358
                      TYPE: PRT ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1358, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Barney, S. APPLICANT: Guthrie, K. APPLICANT: Merutka, G.
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                                                                    US-10-252-136-4
LENGTH: 36
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wald, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Petteway, Stephen R.
Langlois, Albhonse J.
IITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                 1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Score 200; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COFUZZI, LAUER A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SEQ TWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1359
LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 869-9741/8864
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                                                                                                                                                                                                                   OTHER INFORMATION: Core polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 4:
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                                          Gaps
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    Length 36;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
  Score 200; DB 4;
Pred. No. 2.6e-16;
; Mismatches 0;
                                                                            1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Pred. No. 2.6e-16;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/484,223A FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown;
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-267-748-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMISSION
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                            Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                        Petteway, Stephen I
Langlois, Alphonse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                              Sequence 4, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
                                                                                                                                                                                                                                                                                                                                                    Lambert, Dennis M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
Query Match
Best Local Similarity 100.0%; P:
Matches 36; Conservative 0;
                                                                                                                                                                                                                                                                                                                                Barney, Shawn O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
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RESULT

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GENERAL INFORMATION:

APPLICANT: Trimeris, Inc.

TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and

TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and

TITLE OF INVENTION: their use in therapy

FILE REFERENCE: TRM-004

CURRENT APPLICATION NUMBER: US/10/671,282

CURRENT APPLICATION NUMBER: 60/414,439

PRIOR PILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENT NOS: 114

SEQ ID NOS: 114
                                      GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
FILE REPERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 39
LENGTH: 36
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Bublication No. US20050065319A1
GENERAL INFORMATION:
APPLICANT: Baroudy, Bahige M.
TITLE OF INVENTION: Combination Method For Treating Viral Infections
FILE REPREMENT: 1001358
CURRENT APPLICATION NUMBER: US/10/168,295
CURRENT FILING DATE: 2002-06-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 200; DB 4;
Pred. No. 2.6e-16;
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100.0%; Pred. No. 2.6e-16;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Scu-
100.0%; Pre-
0; F
Sequence 39, Application US/10663589
Publication No. US20040063637A1
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Publication No. US20040122214A1
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Best Local Similarity 100.(
Matches 36; Conservative
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Best Local Similarity 100.
Matches 36; Conservative
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ORGANISM: Artificial
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COUNTRY: USA
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Best Local S:
Matches 36,
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APPLICANT: BURRESNE, Robert S.
APPLICANT: BUUDRELLAB, Nissab
APPLICANT: BOUDDIALLAB, Nissab
APPLICANT: ROBITALLE, MAITIN
APPLICANT: MILNER, Peter G.
TITLE OP INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
TITLE OP INVENTION: INFECTION
FILE REPERBNCE: 500862001501/REDC-1512
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: US 09/623,533
PRIOR APPLICATION NUMBER: US 09/623,533
PRIOR PILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/134,406
PRIOR PILING DATE: 1999-05-17
PRIOR PILING DATE: 1999-05-17
PRIOR PILING DATE: 1999-05-17
PRIOR PILING DATE: 1999-05-17
PRIOR PILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 545
SOFTWARE: PATENTING VOING: 545
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100.0%; Score 200; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0;
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100.0%; Score 200; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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                                                                                                                                                                                       TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
PRIOR APPLICATION NUMBER: PCT/USO1/48802
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,657
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 36
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Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Bridon, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darrech L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10950010 Publication No. US20050070475A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-11-066-697-1422
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TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION TO BLOOD
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT APPLICATION NUMBER: US/57,276
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR PAPLICATION NUMBER: 60/153,406
PRIOR PAPLICATION NUMBER: 60/153,783
PRIOR PAPLICATION NUMBER: 60/159,783
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PATENTING DATE: 1999-10-15
LENGTH: 36
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TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-11-066-697-1422
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 200; DB 6;
100.0%; Pred. No. 2.6e-16;
tive 0; Mismatches 0;
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APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: TOTChia, PhD., Timothy E. REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 110, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
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FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 534, Application US/10950010

Publication No. US20050070475A1

GENERAL INFORMATION:

APPLICANT: BRIDON, Dominique P.

APPLICANT: BOUDJELLAB, Nisaab

APPLICANT: BOUDJELLAB, Nisaab

APPLICANT: MILNER, Peter G.

TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL

TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL

TITLE OF INVENTION: LONG LASTING FUSION

TITLE OF INVENTION: UNMERR: US/10/950,010

CURRENT APPLICATION NUMBER: US/10/950,010

CURRENT FILING DATE: 2000-09-05

PRIOR PELLING DATE: 2000-05-17

PRIOR APPLICATION NUMBER: US 60/134,406

PRIOR APPLICATION NUMBER: US 60/134,406

PRIOR APPLICATION NUMBER: US 60/153,406

PRIOR APPLICATION NUMBER: US 60/153,406
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Publication No. US20030186874A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GUIDAT:
APPLICANT:
AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 182; DB 3; Length 46;
Pred. No. 4.4e-14;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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                                                                                                                                                                                                                                                        TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
                                                                                                                                              LENGTH: 46 amino acids
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.9%;
Matches 32; Conservative
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                                                                                                                                                                                                      TYPE: Amino Acid
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US-10-950-010-534
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GENERAL INFORMATION:
APPLICANT: SERRES, Pierre-Francois
APPLICANT: MOSCA, JOSGAT
APPLICANT: MOSCA, JOSGAT
APPLICANT: MOSCA, JOSGAT
TITLE OF INVENTION: TO TARGET CELLS
TITLE OF INVENTION: TO TARGET CELLS
TITLE OF INVENTION: TO TARGET CELLS
FILE REFERENCE: 118761
CURRENT PILLING DATE: 2003-06-10
FRIOR PELLING DATE: 2003-02-11
PRIOR PELLING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/413, 919
PRIOR PILLING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/386,754
PRIOR APPLICATION NUMBER: US 60/386,754
PRIOR APPLICATION NUMBER: US 60/386,754
SRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PALENTIN OF SEQ ID NOS: 72
SEQ ID NO 52
LENGTH. 36
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90.0%; Score 180; DB 4;
Best Local Similarity 86.1%; Pred. No. 5.9e-14;
Matches 31; Conservative 4; Mismatches 1.
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90.0%; Score 180; DB 4;
Best Local Similarity 86.1%; Pred. No. 5.9e-14;
Matches 31; Conservative 4; Mismatches 1;
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION UNBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SEQ ID NO 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 6, 2006, 15:50:31
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                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-10-457-780-52
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*
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1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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US-11-187-687-22
US-11-187-687-22
US-11-187-687-24
US-11-089-426-10
US-10-506-796A-6
US-10-506-796A-7
US-10-506-796A-1
US-10-506-796A-1
US-10-506-796A-1
US-10-506-796A-1
US-11-12-277-34
US-11-112-277-34
US-11-112-277-34
US-11-112-277-34
US-11-112-277-34
US-11-112-277-34
US-11-112-277-34
US-11-112-277-34
US-11-112-277-37
US-11-112-277-37
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US-11-112-277-37
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Maximum Match 100% Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 50
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No.
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Sequence 13381, A Sequence 13388, A Sequence 1322, A Sequence 8659, Ap Sequence 103, App Sequence 103, App Sequence 102, App Sequence 102, App Sequence 3967, App Sequence 3976, App Sequence 39776, App Sequence 3776, App Sequence 12511, App Sequence 12511, App Sequence 12511, App Sequence 12511, App Sequence 101, App Sequence 1056, App Sequence 10566, App Sequence 105666, App Sequence 105666666666666666666666666666666666666	HIV DRUGS	Length 36; Indels 0; Gaps 0;
US-11-045-024-1338 US-11-045-024-1338 US-11-045-024-1922 US-11-045-024-103 US-11-045-024-103 US-11-045-024-103 US-11-045-024-103 US-11-045-024-103 US-11-045-024-102 US-11-045-024-102 US-11-045-024-103 US-11-045-024-101 US-11-045-024-101 US-11-045-024-101 US-11-045-024-101 US-11-045-024-101 US-11-045-024-101 US-11-045-024-101 US-11-045-024-101	ALIGNMENTS 11956A 1 A A. J. IC PROTEINS WITH ANTI-HIV 000 5/10/841,956A -06 468,835	2B 6; 3e-15; 3mwr 36 3mwr 36
43.0 388.5 348.0 34.0 34.0 31.5 31.5 31.5 31.5 31.5 31.5 30.5 30.5 30.5 30.5 30.5 30.5 30.5 30	ESULT 1 S-10-841-956A-1 Sequence 1, Application US/10841956A Publication No. US20050281829A1 GENERAL INFORMATION: APPLICANT: MEAC. ADAM R. APPLICANT: TAN HEHIR, CRISTINA A. APPLICANT: STATTEL, JAMES M. APPLICANT: STATTEL, JAMES M. APPLICANT: BITONTI, ALAN R. TITLE OF INVENTION: FC CHIMERIC PROTEINS FILE REPERBENCE: 08945,003-00000 CURRENT FILING DATE: 2004-05-06 RICH APPLICATION NUMBER: 60/468,835 PRIOR PILING DATE: 2003-05-06 NUMBER OF SEQ ID NOS: 59 SOFTWARE: PATENTIN VOY: 3.2 SOFTWARE: PATENTIN VOY: 3.2 SEG ID NO 1 LENGTH: 36 TYPE: PRT ORGANISM: Human immunodeficiency virus	Query Match Query Match Query Match Best Local Similarity Best Local Similarity 1 YTGITVALLEESQNQCENTEQELLELDKWANLY
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 US-10-841-956A-1 Sequence 1, Ap PUBLICARIT INFORM APPLICANT: TA APPLICANT: P APPLICANT: S APPLICANT: P APPLICANT:	Query Match Best Local 3 Matches 3 Null 2 11-029-003- Sequence 1, Publication GENERAL INFO APPLICANT: TITLE OF INFO TITLE OF INFO TITLE OF INFO

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APPLICANT: Cho, Ho Sung
APPLICANT: Cho, Ho Sung
APPLICANT: Daniel, Thomas O.
APPLICANT: Hays, Anna-Maria
APPLICANT: Hays, Anna-Maria
APPLICANT: Hays, Anna-Maria
APPLICANT: Marian, Troy E.
APPLICANT: Mariani, Roberto
APPLICANT:
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83.3%; Pred. No. 1.7e-15;
tive 5; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MOD_RES
LOCATION: 37
COTATION: 37
COTATION: 37
USEN INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-33
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87.5%; Score 175; DB 7;
Best Local Similarity 83.3%; Pred. No. 2e-15;
Matches 30; Conservative 5; Mismatches
      CURRENT APPLICATION NUMBER: US/11/112,277
CURRENT FILING DATE: 2005-04-22
PRIOR PILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PASKED for Windows Version 4.0
ERG ID NO 33
LENGTH: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 24, Application US/11187687; Publication No. US20060019347A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: T20 Analogue
                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 83.3'
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FUBLICANT: Cho, Ho Sung

APPLICANT: Cho, Ho Sung

APPLICANT: Daniel, Thomas O.

APPLICANT: Marian Amain Amain Amain Applicant: Marian, Roberto

APPLICANT: Mariani, Roberto

CURRENT PELING DATE: 2004-07-21

PRIOR FILING DATE: 2006-07-21

PRIOR FILING DATE: 2005-03-07

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.3
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US-11-112-277-33
US-11-112-277-33
Sequence 33, Application US/11112277
Publication No. US20050267293A1
GENERAL INFORMATION:
APPLICANT: Bousquet-Ganon, Nathalie
APPLICANT: Quralshi, Omar
APPLICANT: Bridon, Dominique P.
TITLE OF INVENTION: CONJUGATES
TITLE OF INVENTION: CONJUGATES
FILE REFERENCE: 500862003700
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Pred. No. 1.6e-15;
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PRIOR APPLICATION NUMBER: 60/539,207
PRIOR FILING DATE: 2004-01-26
PRIOR PELING NUMBER: 60/487,964
PRIOR FILING DATE: 2003-07-17
PRIOR PILING DATE: 2003-07-17
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATCHIN Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/11187687
Publication No. US20060019347A1
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Best Local Similarity 83.3%;
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Best Local Similarity
Matches 30; Conserv
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LENGTH: 36
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APPLICANT: CAROLAN, NOUDUNK1
TITLE OF INVERTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.0006U2
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT PILING DATE: 2004-09-073
PRIOR APPLICATION NUMBER: PCT/US03/07073
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: ALING DATE: 2002-03-06
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NUMBER OF SEQ ID NOS: 9
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APPLICANT: MATOBA, Nobuyuki
APPLICANT: ARNTZEN, CHATLES
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.0006U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1).(36)
COTHER INFORMATION: HIV-1 isolate 593 clone (residues 649-685)
US-10-506-796A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE.

LOCATION: (1). (36)

CTER INDERATION: HIV-1 isolate 1924v3.20 (residues 649-685)
US-10-506-796A-7
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Pred. No. 7.9e-11;
0; Mismatches 1
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Pred. No. 1.4e-10;
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CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: PCT/US03/07073
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 7
SEQ ID NO 7
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92.0%;
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Best Local Similarity 96.0
Matches 24; Conservative
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Best Local Similarity
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APPLICANT: MOR, TSAÉTIF
APPLICANT: MATOBA, Nobuyuki
APPLICANT: MATOBA, Nobuyuki
APPLICANT: MATOBA, Nobuyuki
APPLICANT: MATOBA, Challes
FILE REFERENCE: 01231.0006U2
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT APPLICATION NUMBER: PCT/US03/07073
PRIOR PILING DATE: 2003-03-06
PRIOR PILING DATE: 2003-03-06
PRIOR PILING DATE: 2003-06
NUMBER OF SEQ ID NOS: 9
SOFTHARE: PATOMENT PATOMENT SEQUENCE
SEQ ID NOS: 9
SOFTHARE: PATOMENT SECOND SECO
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                                       TITLE OF INVENTION: FC Fusion Proteins For Enhancing the Immunogenicity of TITLE OF INVENTION: Protein and Peptide Antigens
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COTHER INFORMATION: HIV-1 isolate 98BRRS012 (residues 649-685)
US-10-506-796A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Fused OTHER INFORMATION: polypeptide from pdC-muFC vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 44;
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Pred. No. 5.9e-11;
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Best Local Similarity 84.8%; Pred. No. 6.1e-14;
Matches 28; Conservative 5; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LIHSLIEESQNQQEKNEQELLELDKWASLWNWF 34
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ORGANISM: Human immunodeficiency virus type 1
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                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/089,426
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: US/09/621,268
PRIOR FILING DATE: 2000-07-21
PRIOR PLING DATE: 1999-07-21
PRIOR PLING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10506796A Publication No. US20060013831A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 69.0%;
1 Similarity 96.0%;
24; Conservative
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                                                                                                            FILE REFERENCE: LEX-007
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Best Local Similarity
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LENGTH: 44
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TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
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NAMEKEY: PEPTIDE
LOCATION: (1)..(35)
COTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
US-10-506-796A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JAPELICANT: TRUCKMAILON:
JAPELICANT: MEZO, ADAM R.
JAPELICANT: MEZO, ADAM R.
JAPELICANT: PERES, ROBERT T.
JAPELICANT: STATTEL, JAMES M.
JAPELICANT: STATTEL, JAMES M.
JAPELICANT: BITONIT, ALAN R.
JILLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
FILE REFERENCE: 089455.0003-000000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT PILING DATE: 2004-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PALCHIN Ver. 3.2
SEQ ID NO 3
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0%; Score 120; DB 6; Best Local Similarity 84.0%; Pred. No. 9.8e-09; Matches 21; Conservative 1; Mismatches 3.
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Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
                               THIRE CF ANY MAN AND ANY CONTROLL OF THE REFERENCE: 01231.0006U2
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2004-09-03
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
LENGTH: 36
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ORGANISM: Human immunodeficiency virus
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; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: STATTEL, JAMES
; APPLICANT: STATTEL, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10841956A; Publication No. US20050281829A1; GENERAL INFORMATION:
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Best Local Similarity 72.4'
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; Sequence 3, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
    APPLICANT: MATOBA, Nobuyuki
    APPLICANT: MATOBA, NOBPRIBLY
    FILE REPERBENCE: 01231.000602
    CURRENT APPLICATION NUMBER: US/10/506,796A
    CURRENT FILING DATE: 2004-09-03
    RAIOR APPLICATION NUMBER: 60/362,247
    PRIOR PILING DATE: 2002-03-06
    PRIOR PILING DATE: 2002-03-06
    NUMBER OF SEQ ID NOS: 9
    SOFTWARE: PATORIN Version 3.2
    SEQ ID NOS: 9
    SEQ ID NOS: 9
    SEQ ID NOS: 9
    SEQ ID NOS: 9
APPLICANT: MOR, Teafrir
APPLICANT: MATOBA, Nobuyuki
APPLICANT: MATOBA, Nobuyuki
APPLICANT: MATOBA, Nobuyuki
APPLICANT: MATOBA, Charles
ITILE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.0006402
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT APPLICATION NUMBER: PCT/US03/07073
PRIOR APPLICATION NUMBER: EC1/US03/07073
PRIOR APPLICATION NUMBER: 60/362,247
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 35
WONDER OF SEQ ID NO 1
LENGTH: 35
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COTATION: (1)..(35)

CHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)

US-10-506-796A-1
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Pred. No. 3.2e-10;
1; Mismatches 1; Indels
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66.0%; Score 132; DB 6;
Best Local Similarity 92.0%; Pred. No. 3.3e-10;
Matches 23; Conservative 1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 66.0%;
l Similarity 92.0%;
23; Conservative 1
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APPLICANT: MATORA, Nobuyuki
APPLICANT: ARNTZEN, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BOUSQUEE Gagnon, Nathalie
APPLICANT: Quzaishi, Omar
APPLICANT: Quzaishi, Omar
APPLICANT: Bridon, Dominique P.
TITLE OF INVENTION: CONJUGATES
TILE REPRESENCE: 500862003700
CURRENT APPLICATION NUMBER: US/11/112,277
CURRENT APPLICATION NUMBER: US 60/565,228
PRIOR FILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastESEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%; Score 119; DB 7; Length 40; 72.4%; Pred. No. 1.5e-08; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.5%; Score 119; DB 7; Length 39; Best Local Similarity 72.4%; Pred. No. 1.4e-08; Matches 21; Conservative 4; Mismatches 4; Indels
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COCATION: 40
COTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-34
                 FILE REFERENCE: 08945.0007-01000
CURRENT APPLICATION NUMBER: US/11/029,003
CURRENT FILING DATE: 2005-01-05
FRIOR APPLICATION NUMBER: 60/539,207
PRIOR FILING DATE: 2004-01-26
PRIOR FILING DATE: 2004-01-26
PRIOR PILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/469,600
PRIOR FILING DATE: 2003-07-17
PRIOR PILING DATE: 2003-07-17
PRIOR FILING DATE: 2003-05-06
SUGTWARE: PATON NUMBER: 60/469,600
PRIOR FILING DATE: 2003-05-06
SUGTWARE: PATON NUMBER: 60/469,600
PRIOR FILING DATE: 2003-05-06
SUGTWARE: PATON NUMBER: 60/469,600
PRIOR FILING DATE: 2003-05-06
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                                                                                                                                                                                                                                                                                                                                                            i LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-029-003-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-112-277-34
; Sequence 34, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
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OTHER INFORMATION: T1249 Analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 72.4<sup>3</sup>
Matches 21; Conservative
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8 LLEESQNQOEKNEQELLELDKWANLWNWF 36

Search completed: March 6, 2006, 15:54:21 Job time : 10 Becs

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n 5.1.7	- 2006 Biocceleration Ltd.
version	- 2006
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

March Run on:

6, 2006, 16:12:57 ; Search time 117.333 Seconds (without alignments) 134.809 Million cell updates/sec

Title: Perfect score:

US-09-809-060A-3 36 1 YIGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

2443163 segs, 439378781 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

geneseqp2003as:*geneseqp2003bs:* A_Geneseq_21:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp20008:* geneseqp2001s:* geneseqp2004s:* geneseqp2002s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aar67699 DP-178 ho	Aar98400 Peptide c	Aaw17013 DP-178-li	Aab54787 HIV antiv	Aab92246 Virus rel	Aab78239 Core poly	Aab78240 Core poly	HIV	Abb02832 Viral cor	Abb02831 Viral cor	Aag67041 HIV-1 gp4	Viral	Abb01247 Viral DP1	Aau13793 DP178-lik	Aau13792 DP178-lik	. Aau14013 DP178 hom	_	Ade02851 Hybrid po		Abol0165 HIV1-RF g	Adn06924 Peptide #	-	Ady71494 HIV-1 tra	Aay22837 SEQ ID NO
SUMMARIES	, OI	AAR67699	AAR98400	AAW17013	AAB54787	AAB92246	AAB78239	AAB78240	AAU70181	ABB02832	ABB02831	AAG67041	ABB01246	ABB01247	AAU13793	AAU13792	AAU14013	AA018773	ADE02851	ADE02852	ABO10165	ADN06924	ADS87259	ADY71494	AAY22837
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	* Query Match Length DB	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	269
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Abg68308 Envelope Abu57715 Human imm Aaw43074 HIV-1 gpl Aap70175 Sequence		Adu68214 gp41 ecto Adx39678 HIV Env p Aar67698 DP-178 ho AAr98399 DD185 cor	DP-17 HIV-1 DP178 Human	Adk66261 Human imm Adu80506 Transmemb Adz40264 HIV-1 gp4 Aap61514 Sequence Aaw89325 HIV-1 env
ABG68308 ABU57715 AAW43074 AAP70175	ADX39688 AAP80966 AAY89838 AAY89839	ADU68214 ADX39678 AAR67698 AAR98399	AAW17012 AAG67040 AAU14012 ADK66257	ADK66261 ADU80506 ADZ40264 AAP61514 AAW89325
269 5 269 6 861 2 865 1	865 9 866 1 35 3	849 36 36 36 36	3 3 3 3 3 3 3 3 4 4 4 7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	45 48 8 48 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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36 36 36	36 31 31	27 26 26	2 0 0 0 0 7 7 7 7 8	7 7 7 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
25 26 27 28	33 32 32 32	6 6 8 6 4 8 6	1 E E E 4	4444 10640

ALIGNMENTS

antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI; human immunodeficiency virus; transmembrane protein; gp41; alpha helix; DP-178 homologue derived from HIV-1 RF has antiviral activity. AAR67699 standard; peptide; 36 AA. (first entry) leucine zipper; DP-185. (revised) (revised) 24-AUG-1995 AAR67699; RESULT 1 AAR67699

Human immunodeficiency virus; (RF isolate).

WO9428920-A1

22-DEC-1994.

94WO-US005739 07-JUN-1994; 93US-00073028 07-JUN-1993;

(UYDU-) UNIV DUKE.

Lambert DM; Barney SO, Wild CT, Bolognesi DP, Matthews TJ, Petteway SR;

WPI; 1995-036105/05.

Computer search generated synthetic peptides - are inhibitors of HIV transmission.

Example; Fig 1; 182pp; English

This peptide is isolated from HIV-1 isolate RF, and is a homologue of the peptide DP-178. DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalent protein-protein interactions, and possess anti-viral activity. The peptide inhibits transmission to uninfected cells, and can also be used as type and/or subtype specific diagnostic tools. (Updated on 25-MAR-2003 to correct PN

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AAW17012-W17016 are DP-178 homologues that are useful in the treatment of HIV infection. DP-178 is a peptide corresponding to residues 638-673 of HIV type 1 glycoprotein 41 (gp41) transmembrane protein. DP-178 and its derivatives/homologues are used in combination with a therapeutic agent, e.g a reverse transcriptase, viral protease, cytokine, glycosylation or viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides work by inhibiting viral replication or inhibiting transmission. They may also be used in vaccines for protecting against HIV infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compans. contg. DP-178 or DP-107 in combination with other therapeutic agent - useful for treatment of HIV infection, esp. by inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Long lasting fusion peptide inhibitor; viral infection; antiviral; antifusogenic; mobile blood component; measles virus; MeV; SIV; sinian immunodeficiency virus; human parainfluenza virus; HPVV; human respiratory syncytial virus; human immunodeficiency virus; HIV.
                                                                                                                                                                                                          HIV; SIV: human; simian immunodeficiency virus; glycoprotein 41;
transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;
replication; transmission.
                                                                                                                                                                    DP-178-like peptide useful for treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV antiviral activity exhibiting peptide SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                           Human immunodeficiency virus 1; RF isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replication or transmission of HIV.
                         AAW17013 standard; peptide; 36 AA.
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                                                                                                         (revised)
(first entry)
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Best Local Similarity 100.
Marches 36; Conservative
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01-JUL-1997
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05-MAR-2001
                                                                 AAW17013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAR98398-408 represent peptides which exhibit antifusogenic activity, antiviral capability and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. These peptides are recognised by the ALMOTIS, 107x178x4 and PLZIP search motifs. These peptides may be used to inhibit the transmission of a virus, pref. HIV, influenza virus, or heparitis B virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an isolated peptide recognised by an ALLMOTIS, 107x178x4 or PLZIP sequence search motif.
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antifusogenic activity, antiviral capability, coiled-coil peptide, ALLMOTIS; 107x178x4; PLZIP search motif, viral transmission; HIV; influenza virus; hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.
                                                                                    Length 36
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100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                   100.0%; Score 36; DB 2; Lengtu .v. 100.0%; Pred. No. 2e-27; wismarches 0; Indels
field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                         1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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                                                                                                                                                                                                                                                                                                         AAR98400 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus 1.
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Petteway SR, Langlois AJ;
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(first entry)
                                                                                                   Best Local Similarity 100.
Matches 36; Conservative
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                                          Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36 AA;
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17-FEB-1997
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                                                                                  Query Match
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RESULT 3

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Length 36; IndelB

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The present invention describes a modified therapeutic peptide (1) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide componed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic; antiinflammatory; hybrid polypeptide; colled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intracellular uptake and interference with physiological processom AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                               Milner PG, Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 36; DB 4; Length 36; 100.0%; Pred. No. 2e-27; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 662-663; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB78239 standard; peptide; 36 AA
                                                                                                                                                     99US-0134406P.
99US-0153406P.
99US-0159783P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0-JUL-2000; 2000WO-US018772.
                                                                                                       L7-MAY-2000; 2000WO-US013576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Core polypeptide T1407.
                                                                                                                                                                                                                                                                                                                  Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                              (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200103723-A1
WO200069900-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                     17-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                           15-0CT-1999;
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                                                23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB78239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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AAB78239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a modified anti-viral peptide (I)

comprising a peptide that exhibits anti-viral activity and a reactive
group which is reactive with amino groups, hydroxyl groups, or thiol
groups on blood components to form stable covalent bonds. (I) has anti-
cviral and anti-fusogenic activities. (I) inhibits viral infection of
cells by inhibiting cell-cell fusion or free virus infection or to reduce
the level of membrane fusion events between two or more entities, e.g.,
virus-cell or cell-cell, relative to the level of membrane fusion that
cocurs in the absence of the peptide. (I) is useful in the treatment of
patients who are suffering from viral infection, e.g. HIV, RSV, HBIV,
MeV, and SIV. (I) may be administered prophylactically to previously
uninfected individuals. This is useful in cases where an individual has
components of the blood, such as immunoglobin, serum albumin, red
lived components of the activity is extended for days to weeks.
This is due to improved stability in vivo and a reduced ausceptibility to
peptidase or protease degradation. This minimises the need for more
frequent, or even continual, administration of the peptides. AAB54784
AAB55431 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                            A modified peptide and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds useful for treatment of viral infections, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                          Boudjellab N, Robitaille M, Milner PG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YIGIIYNLLEESONQOEKNEQELLELDKWANLWWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 173-174; 211pp; English.
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Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human immunodeficiency virus.
                                                                                                                                                       17-MAY-2000; 2000WO-US013651
                                                                                                                                                                                                        99US-0134406P
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                                                                                                                                                                                                                                                                                                                                          Dufresne RP,
                                                                                                                                                                                                                                                                                       (CONJ-) CONJUCHEM INC.
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                                                WO200069902-A1.
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                                                                                                    23-NOV-2000
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Guthrie KI,
                                                                                    Guthrie KI,
                           (TRIM-) TRIMERIS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 AA;
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                                                                                                                                                                                                                                                               polypeptide.
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                                                                                    Barney S,
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AAB 78240
ID AAB 7
XX
AAC AAB 7
XX
DT 19-A
DT 19-A
DY COFE
XX
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The present sequence is a core polypeptide which may be linked to an anovel hybrid polypeptide. The hybrid polypeptide exhibited to form a novel hybrid polypeptide. The hybrid polypeptide exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide. The hybrid and core polypeptides can be used for modulating tusgenic events and intracellular processes involving coiled coil peptide interactions. Other uses include preventing, treating and/or alagnosing disporders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus, respiratory syncytial virus, Epstein Barr virus, hepatilis B virus, Mason-Pfizer virus and reduces the clearance rate of therapeutic peptides, which increases their effects. In addition, this increases the sensitivity of the diagnostic
                                                                                                                                                                                             New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core
Lambert DM;
Anwer MK,
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 58; 151pp; English.
Merutka G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    procedure in which they are used
                                                                                           WPI; 2001-147136/15
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                                        Gaps
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100.0%; Score 36; DB 4; Length 36; 100.0%; Pred. No. 2e-27; ive 0; Mismatches 0; Indels
                                                                      1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                    36; Conservative
                 Best Local Similarity
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Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic; antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.
1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                                   AAB78240 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                19-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Core polypeptide T1408.
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10-JUL-2000; 2000WO-US018772.

Immunogenic composition for inhibiting HIV infection, comprises viral envelope protein or its fragment exterior to viral membrane, a stabilizing peptide, and, optionally, viral cell surface receptor or its WPI; 2001-626098/72. fragment.

Lambert DM;

Anwer MK,

Merutka G,

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The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid confered sexibites enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system It is used to increase the in vitro or ex vivo half-life of the core polypeptide. The hybrid and core polypeptides can be used for modulating fusogenic events and intracellular processes involving coiledcoil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg (usion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side efficacy and minimises the incidence and severity of adverse side efficacy and minimises the incidence and severity of adverse side efficacy and minimises the incidence and severity of the diagnostic
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anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120,
alpha-helical region; ectodomain.
                             New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 36; DB 4; 100.0%; Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                       Disclosure; Page 58; 151pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  procedure in which they are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAR-2000; 2000US-0189981P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36 AA;
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                                                                                                    polypeptide.
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Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
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                                                                                                                                                                                                                                                    Viral core polypeptide, SEQ ID NO: 1359.
                                                                                                                                                                                                      ABB02832 standard; peptide; 36 AA
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                                                                                                                                                                                                                             (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                               (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-514829/56.
                                                                                                                             Sequence 36 AA;
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06-AUG-2003
03-JAN-2002
                                                                                                                                                                                                                                                                                                             07-SEP-2001.
                                                                                                                                                                                                                                                                           infection.
                                                                                                                                                                                                                                                                                                                                                                                             infection
                                                                                                                                                                                                                  ABB02832;
                                                                                                                                                                                                                                                                                      Viruses.
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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-633 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV specification. The present sequence is a peptide provided in the specification. (Updated on 06-bUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat regions of RSV) infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection. In a cell. They may also be used to inhibit HIV sepecification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 36; DB 4; Length 36; Local Similarity 100.0%; Pred. No. 2e-27; les 36; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YTGIIYNLLEESONQOEKNEGELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB02831 standard; peptide; 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(revised)
(first entry)
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                                                                                                                                                                                                                                                                                        Sequence 36 AA;
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Matches
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                                                                        The Infortion Feature of Mich Larget regions of viral envelope proteins auch as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-1 (human immundeficiency virus 1). Sequences ANUTO19-ANUTO198 and AAU70677-AAU70743 represent stabilising peptides modelling the alphablical regions of the ectodomain of the HIV-1 transmembrane protein to stabilise fusion-active intermediate structures, which can be used as vaccine immunogens. Immunogenic compositions comprise a viral envelope protein or its fragment exterior to the viral membrane, a stabilising peptide to disrupt formation of structural intermediates necessary for viral fusion and entry, and optionally, a viral cell surface receptor or its fragment. The stabilising peptide is capable of associating with the structure. Antibody binding assays are used to determine the ability of immunogen vaccines to generate an immune response to various forms of envelope. Viran neutralisation assays can be used to characterise the antibody response raised against HIV-1 gp41 domains. The sequences and methods are useful for inhibiting antibodies
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                                                              The invention relates to methods of generating immunogens that elicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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            6; Page 45; 84pp; English.
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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-

Disclosure; Page 525; 587pp; English.

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RESULT 11

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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and S58-585 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV intection. The present sequence is a peptide provided in the specification. (Updated on 06-40G-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                      Human immunodeficiency virus, HIV, respiratory syncytial virus, RSV, virucide, heptad repeat region, transmembrane protein, gp41, HR1, HR2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
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100.0%; Pred. No. 2e-27; "**=marche8 0; Indels
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                                                                                                                                                                Viral DP178/107-like region peptide T1407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 58; 587pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB01247 standard; peptide; 36 AA.
  ABB01246 standard; peptide; 36
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06-AUG-2003
03-JAN-2002
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                                                                                                                                                                                                                                                                                        Viruses.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
infection; DP185.
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                                     100.0%; Score 36; DB 4; Length 36; 100.0%; Pred. No. 2e-27; ive 0; Mismatches 0; Indels
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                                                                                                                      1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF
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(first entry)
                                     Query Match 100.
Best Local Similarity 100.
Matches 36; Conservative
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Sequence 36 AA;
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Gaps

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11-SEP-2003 (revised)

RESULT 12 ABB01246

Matches

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Length 36;

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21-NOV-2001 (first entry)
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Matches 36; Conservative
                                                                                            (TRIM-) TRIMERIS INC
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                                                               09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                        Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus infection.
                                                                        Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
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                                           Viral DP178/107-like region peptide T1408
                                                                                                                                                                                                                                                                                                                         Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DP178-like/DP107-like peptide T-1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 58; 587pp; English.
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                                                                                                                                                                                                                                                                                                                              MK,
(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                              Delmedico
                                                                                                                                                                                                                                                                                              (TRIM-) TRIMERIS INC
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06-AUG-2003
            03-JAN-2002
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                                                                                                          infection.
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                                                                                                                                       Viruses.
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AAU13793
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activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 619-673 of the transmembrane protein gp41 from human immunodeficiancy virus I (HIV-1) solate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-ILAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, pequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to peptides which exhibit anti-retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a compound that inhibits the formation of or disrupts DP107/DP178 complex, especially compounds with antifusogenic, anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                            Merutka G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 36; DB 4; Length 36; 100.0%; Pred. No. 2e-27; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "N-terminal is substituted by Ac"
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                                                                                                                                                                                                                                                            Lawless MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1; isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP178-like/DP107-like peptide T-1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 77; 259pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                            Lackey JW, Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU13792 standard; peptide; 36 AA.
                                                                                  99US-00350841.
05-JUL-2000; 2000WO-US035727
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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise activity. The peptides of the invention (AAU12559-AAU14009) comprise to bpine DB108 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAT. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-LLAI. The invention also relates to a method of identifying compounds that inhibit the corresponds to a method of identifying compounds that inhibit the corresponds to a peptiden also performance of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, committing a intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence corresponds to particularly HIV, transmission to uninfected cells. The present sequence
                                                                                                                                                                                                                               Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex.
                                                                                                                                          Lawless MK, Merutka G;
                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 77; 259pp; English.
                                                                                                                                        Erickson JB,
05-JUL-2000; 2000WO-US035727.
                                              99US-00350841.
                                                                                                                                     Jeffs P, Lackey JW,
                                                                                          (TRIM-) TRIMERIS INC
                                                                                                                                                                                    WPI; 2001-442157/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36 AA;
                                           09-JUL-1999;
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Gaps ö Query Match 100.0%; Score 36; DB 4; Length 36; Best Local Similarity 100.0%; Pred. No. 2e-27; Matches 36; Conservative 0; Mismatches 0; Indels

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1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36

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6, 2006, 16:19:05

Search completed: March Job time : 118.333 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 6, 2006, 16:19:28 ; Search time 19 Seconds
(without alignments)
182.305 Million cell updates/sec

US-09-809-060A-3 36 Title: Perfect score:

Sequence:

1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 segs, 96216763 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

pir 80:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result . No.	Score	Query	Query Match Length	DB	ID	Description
	26	72.2	. &	-	VCLJVL	env polyprotein pr
~	23		80	Н	VCLJA2	
m	21	58.3	357	~	S21994	protein
4	21	58.3	357	~	S21996	protein
2	21		443	~	C41621	env polyprotein P
9	21		847	~	T09448	envelope glycoprot
7	21	58.3	847	~	S13289	env protein - huma
æ	21		851	~	S33985	env polyprotein -
σ	21		854	N	S13288 .	env protein - huma
10	. 21	8		Н	VCLJ3W	env polyprotein pr
11	21	8		Н	VCLJH3	
12	21	œ.		Н	VCLJSC	
13	21	ω.		Н	VCLJLV	env polyprotein pr
14	19	52.8		~	S21992	protein
15	19	'n		~	S21998	
16	16	4		?	S54384	envelope polyprote
17	16	4	4 855	Н	VCLJZR	env polyprotein pr
18	16	44.4		Н	VCLJMIN	env polyprotein pr
19	15	41.7	357	7	\$22004	proteir
20	15	41.7	357	7	S22006	protein
21	13	36.1	357	7	S21990	envelope protein g
22	13	36.1		ч	H44001	
23	13	36.1		7	T12016	envelope glycoprot
24	12	33.3		~	S70417 .	
25	12	33.3		7	S22000	protein
56	12	33.3		~	S22002	envelope protein g
27	12	33.3		N	A41621	
28	12	33.3	454	~	B41621	polyprotein
53	12	33.3	1 729	н	VCLJKX	env polyprotein pr

env polyprotein pr env polyprotein pr		env polyprotein pr	env polyprotein -	lope	catechol oxidase (catechol oxidase (catechol oxidase (envelope polyprote	envelope polyprote	hypothetical prote	cysteine synthase	hypothetical prote	glutamate dehydrog	protoporphyrin IX
VCLJKB A44963	VCLJH4	VCLJND	VCLJBR	T01672	T03682	533540	T07097	JU0266	JT0954	T46082	C90179	T19415	G69933	T01790
ч.	Н	н	Н	7	~	-	7	0	~	7	Ņ	7	7	0
861	898	846	852	859	592	296	599	136	136	198	297	425	426	426
33.3	27.8	25.0	25.0	25.0	22.2	22.2	22.2	19.4	19.4	19.4	19.4	19.4	19.4	19.4
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30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)

N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004

Accession: A03974

RiMuesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J. Nature 313, 450-458, 1985
Astitle: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovis A; Reference number: A93355; MUID:85111157; PMID:2982104

;Molecule type: DNA ;Residues: 1-856 <MUE> ;Cross-references: UNIPROT:P03376; UNIPARC:UP1000012A01F; GB:K02083; NID:9555008; PIDN:J

C.Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F;1-300 Domain: signal sequence #steatus predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F;812-856/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict

Gaps ö 72.2%; Score 26; DB 1; Length 856; 100.0%; Pred. No. 1.2e-17; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0°
Matches 26; Conservative

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10 RESONOGEKNEGELLELDKWANLWNW 35

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env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2) N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #text_change 09-Jul-2004

Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi Accession: A03976

Science 227, 484-492, 1985
A; Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2). A; Reference number: A04003; MUID:85090453; PMID:2578227

Accession: A03976

A,Molecule type: DNA A,Rosidues: 1-855 <SAN> A,Crestdues: 1-855 <SAN> A,Genetics: UNIPROT:P03378; UNIPARC:UPI000012A00F; GB:K02007; NID:g328658; PIDN:/

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148 EESONOOEKNEOELLELDKWA 168
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                      Best Local Similarity 100.
Matches 21, Conservative
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                                                                C; Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot F:1-10/Domain: signal sequence #status predicted <SIG>
F:3-150/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TWM>
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,388,364,388,394,400,408,445,458
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            envelope protein gp120/gp41 - human immunodeficiency virus type 1
C;Species: human immunodeficiency.virus type 1, HIV-1
A;Variety; isolate 27B
C;Date: 20-Feb-1995 #Bequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S21994; S70421
C;Accession: S21994; S70421
B;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         envelope protein gpl20/gp41 - human immunodeficiency virus type 1 (patient 27L)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Species: buman immunodeficiency virus type 1, HIV-1

C;Accession: 570422; 521996

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

A;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrance number: S70412;

A;Accession: S70422
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-373 cST2>
A;Residues: 1-373 cST2>
A;Cross-references: UNIPROT: Q78119; UNIPARC: UPI0000104EC6; EMBL: X61356; NID: g60181; PIDN
A;Experimental source: patient 27L
A;Note: submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Restdues: 1-357 <STEL>
A;Cross-references: UNIPROT: Q78118; UNIPARC: UPI0000178606; EMBL: X61355; NID: g60179; PIDN R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
A;DIS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebra; Reference number: S70417; MUID: 92144209; PMID: 1736940
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-140, XX,142-312, XX,314-357 <STE2>
A;Cross-references: UNIPARC:UPIO000FF05F; EMBL:X61355; NID:g60179
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                          Query Match 63.9%; Score 23; DB 1; Length 855; Best Local Similarity 100.0%; Pred. No. 1e-14; Matches 23; Conservative 0; Mismatches 0; Indels
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Pred. No. 3.9e-13;
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100.0%; Pred. No. ...
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                                               type E retrovirus env polyprotein
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              A;Gene: env
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A,Molecule type: DNA
A,Residues: 1-443 <BUR>
A,Residues: 1-443 <BUR>
A,Cross-references: UNIPROT:Q80023; UNIPARC:UPI0000104256; GB:M77230; NID:g328631; PIDN:/
A,Note: this virus was isolated from the mother's sexual partner
C;Genetics:
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C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
C;Reywords: AIDS; capsid protein gpl20 (fragment) #status predicted <GPl>
F;252-443/Product: coat protein gp41 (fragment) #status predicted <GPl>
F;254-443/Product: coat protein gp41 (fragment) #status predicted <GPl>
F;424-443/Domain: transmembrane #status predicted <TMN>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: can
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R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A. Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity A;Reference number: A41621; MUID:92107924; PMID:1763038
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                                                                                                                                                                                                                                                                                                                                                                                          env polyprotein P - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11.Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                         Gaps
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                                         Indels
red. No. 3.9e-13;
Mismatches 0;
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Statuus: preliminary: translated from GB/EMBL/DDBJ
A;Roaicule type:
A;Residues: 1-847 <PAN>
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09-Jul-2004

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C;Accession: A24774
R;Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, B.£
Cell 45, 637-648, 1986
A;Title: Identification and characterization of conserved and variable regions in the envalence number: A24774; MUID:86218077; PMID:2423250
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A; Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; MUID:85111123; PMID:2578615
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C'Keywords: AIDS; capaid protein; coat protein; glycoprotein; immunodeficiency; polyprote
C'Keywords: AIDS; capaid protein; coat protein els cards
F;1-30 Domain: aignal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-86/Fproduct: transmembrane glycoprotein #status predicted <TMM>
F;812-86.141,156,140,146,140,130,234,241,262,276,289,295,301,332,335,386,392,397,406,
F;81,165,141,156,140,146,170,816/Binding site: carbohydrate (Asn) (covalent) #status predict
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C; Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F; 1-29/Domain: signal sequence #status predicted <SIG>
F; 3-201/Product: coat protein gp120 #status predicted <GP1>
F; 502-847/Product: coat protein gp41 #status predicted <GP2>
F; 87, 134, 140, 151, 155, 183, 197, 234, 241, 262, 276, 289, 295, 331, 338, 354, 360, 390, 394, 404, 447, 459,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Molecule type: DNA
;Residues: 1-856 <STA>
;Cross-references: UNIPROT:P31872; UNIPARC:UP1000012A024; GB:K03455; GB:M38432; NID:g190
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                                                                                                                                                                                                                N/Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change
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A; Residues: 1-856 <RAT>
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VCLJSC
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env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13289
R;O'Strien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.R.
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gpl20
A;Accession: S13289
A;Accession: S13289
A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-654 <08R>
A;Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:O90178; UNIPROT:Q78243; UNIF
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C. Species: human immunodeficiency virus type 1, HIV-1
C. Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C. Accession: S13288
R.O. Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.R. Nature 348, 69-73, 190
A. Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 A; Reference number: S13288; MUID:91043044; PMID:2172833
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A,Residues: 1-851 «CAR»
A,Rcoss-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:g60192;
C,Superfamily: type E retrovirus env polyprotein
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33985
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Reference; S33985
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Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels
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A;Residues: 1-847 <OBR>
A;Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B
C;Superfamily: type E retrovirus env polyprotein
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100.0%; Pred. No. 8.9e-13;
ive 0; Mismatches 0;
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Pred. No. 9e-13;
0; Mismatches 0
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C;Superfamily: type E retrovirus env polyprotein; glycoprotein; immunodeficiency; polyprot
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
E;13.00 coat signal sequence #status predicted <SXT>
F;31.516/Product: exterior membrane glycoprotein #status predicted <TMM>
F;517.861/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Home sapiens (man)
A;Note: host Home sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C;Accession: B28922
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta Virology 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-861/Product: env polyprotein #status predicted <EPP>
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396
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A;Residues: 1-861 <WAL>
A;Cross-references: UNIPROT:P03377; UNIPARC:UP1000012A013; GB:K02013; NID:g326417; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-la) N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-l A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A03975 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A03975 #sequence_revision 0.; Cole, S.; Alizon, M. Cell 40, 9-17, 1985 A;Title: Nucleotide sequence of the AIDS virus, LAV. A;Reference number: A90866; MUID:85099333; PMID:2981635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.3%; Score 21; DB 1; Length 861 Best Local Similarity 100.0%; Pred. No. 9.1e-13; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-861 <GUR>
A;Cross-references: UNIPARC:UPI0000174A39
C;Genetics:
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A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrony. RiReference number: S70417; MUID:92144209; PMID:1736940
A;Recession: S70424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <ST2>
A;Cross-references uNIPROT:Q78112; UNIPARC:UPI0000107A48; EMBL:X61358; NID:g60177; PIDN: A;Experimental source: patient 22
A;Note: submitted to the EMBL Data Library, July 1991
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   envelope protein gp120/gp41 - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

A;Variety: isolate 28

C;Auciety: isolate 20-genence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S21998; S70425

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

aubmitted to the EMBL Data Library, July 1991

A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determir

A;Reference number: S21990
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A;Cross-references: UNIPARC:UPI00000FE72C; EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:
C;Superfamily: type E retrovirus env polyprotein
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A;Title: Distinct nomilation-
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100.0%; Pred. No. 3.5e-11;
tive 0; Mismatches 0;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=86218077; PubMed=2423250; DOI=10.1016/0092-8674(86)90778-6;
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
"Identification and characterization of conserved and variable regions
in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";
                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (isolate RF/HAT) (HIV-1).
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Last sequence update)
13-SEP-2006 (Rel. 48, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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R HSSP; P04578; 1DLB.
SMR; P04579; 549-635.
R HIV, M17451; ENV$RF.
R InterPro; IPR000328; Env GP41.
R InterPro; IPR000328; Env GP41.
R Feam; PF00515; GP120.
R Pfam; PF00515; GP120.
R Pfam; PF00515; GP41; 1.
R AIDS; Capsid protein; Glycoprotein; Polyprotein; Signal; Structural protein; Transmembrane.
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               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Human immunodeficiency virus 1.
Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;
Prices I.L., Soarces M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G., Gouvea M.I.F.S., Guimarzes M.A.M., Do Oliveira F.E., Magnanini M.M.F., Brindeiro R.M., Tanuri A.;
Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naive, infected individuals in the army health service of Rio de Janeiro, Brazil.";
J. Clin. Microbiol. 42:426-430(2004).
EMBL, AY286707, AAQ68133.1; -; Genomic_RNA.
SNR; Q6WH26; 1-105.
GO; GO:0016021; C:integral to membrane; IEA.
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     91.7%; Score 33; DB 2; Length 122;
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ive 0; Mismatches 0; Indels
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ive 0; Mismatches 0; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                 81 IIYNLLEESQNQQEKNEQELLELDKWANLWNWF 113
                                                                                                                     4 IIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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Q4VUS2 9HIV1 PRELIMINARY;
Q4VUS2;
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Matches 33, Conservative
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Q6WH26;
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NCBI_TaxID=11676;
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EMBL, AR307734; AAL08795.1; -; Genomic_DNA.

HSSP, P04674; LJAU.

SMR; O90047; 1-105.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.

PEam; PF00517; GP41; 1.
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Matches 36; Conservative
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NUCLEOTIDE SEQUENCE.
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SEQUENCE 122, AA;
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MEDLINES-1180199; Pubmed=11724274; DOI=10.1023/A:1011812810397;

Caride B., Hertoge K., Larder B., Dehertogh P., Brindeiro R.,

Machado E., de Sa C.A.M., Eyer-Silva W.A., Sion F.S., Passioni L.F.C.,

Menezes J.A., Calazans A.R., Tanuri A.;

"Genotypic and phenotypic evidence of different drug-resistance

mutation patterns between B and non-B subtype isolates of human
immunodeficiency virus type I found in Brazilian patients failing
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                                                                                                                                                                                                                                                           Length 122;
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                                                                                                                                                                                               122 AA; 14758 MW; B2F2785E75F8427E CRC64;
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Virus Genes 23:193-202(2001).
EMBL, AF165535; AAF08480.1; -; Genomic_DNA.
EMBL, AF165535; AAF08480.1; -; Genomic_DNA.
EMBL; P12488; 11M7.
SMR; Q9Q1W9; 1-105.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
GO:0005198; F:structural molecule activity; IEA.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Envelope glycoprotein (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                    88.9%; Score 32; DB 2; Li
100.0%; Pred. No. 3.6e-23;
iive 0; Mismatches 0;
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                              InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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1D 053138 9HIV1 PRELIMINARY;
AC 053138;
DT 13-SEP-2005 (TREMBLrel. 31,
DT 13-SEP-2005 (TREMBLrel. 31,
DT 13-SEP-2005 (TREMBLrel. 31,
DT Name-9p41;
ON Name-9p41;
OS Human Immunodeficiency virus
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QQQIW9;
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                                                                                          Envelope protein.
NON TER 122
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                                                                                              Menzo S., Castagna A., Monachetti A., Hasson H., Danise A., Carini E., Bagnarelli P., Lazzarin A., Clementi M.; "Genotype and phenotype patterns of human immunodeficiency virus type I resistance to enfuvirtide during long-term treatment."; Antimicrob. Agents Chemother. 48:3253-3259(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.
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Korber B.T., Wolinsky S.M., Moore J.P.;
Genetic and phenotypic analyses of human immunodeficiency virus ty I secape from a small-molecule CCRS inhibitor.";
J. virol. 78:2790-2807(2004).
EMBL; AX357545; AAR00902.1; -; Genomic_DNA.
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Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ964909; CAI79657.1; -; Genomic_RNA.
                                                                                                                                                                                                                                                                                                  143 143 AA; 16814 MW; 86046F46914618F9 CRC64;
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PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
                                                                                  PubMed=15328081; DOI=10.1128/AAC.48.9.3253-3259.2004;
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SWR; QGUYP3; 82-162, 194-490, 538-624.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0001998; F:estructural molecule activity; IEA.

InterPro; IPR000328; Env GP41.

InterPro; IPR000777; GP120.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 2.1e-22;
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AIDS; Envelope protein; Transmembrane.
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PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;

PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;

Ruhman S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,

Ruhman S.E., Strizki, J.M., Riley J., Baroudy B.M., Wilson I.A.,

Rorber B.T., Wolinsky S.M., Moore J.P.;

"Genetic and phenotypic analyses of human immunodeficiency virus type
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"J. Virol. 78:2790-2807(2004).

"J. Vir
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000713; Env GP41.
InterPro; IPR00077; GPIZO.
Pfam; PF00516; GP120; 1.
Pfam; PF00516; GP120; 1.
AIDS; Envelope protein; Transmembrane.
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OGIVPB; BHIV1 PRELIMINARY; PRT; 849 AA.
OGUVPB;
OS-JUL-2004 (TrEMBLrel. 27, Created)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Envelope glycoprotein (Fragment).
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100.0%; Pred. No. 2.1e-22;
iive 0; Mismatches 0;
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100.0%; Pred. No. 2.1e-22;
ive 0; Mismatches 0;
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Envelope glycoprotein (Fragment).
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PUDMed:14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
Ruhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
Korber B.T., Wolinsky S.M., Moore J.P.;
"Genetic and phenotypic analyses of human immunodeficiency virus type 1 escape from a small-molecule CCRS inhibitor.";
J. Virol. 78:2790-2807(2004).
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PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
Ruhmann S.E., Pugach P., Kunetman K.J., Taylor J., Stanfield R.L.,
Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
Korber B.T., Wolinsky S.M., Moore J.P.;
"Genetic and phenotypic analyses of human immunodeficiency virus type
1 escape from a small-molecule CCRS inhibitor.";
J. Virol. 78:2790-2807(2004).
BRNBL, AY357763; AR800900.1; -; Genomic_DNA.
HSSP; PO4578; 194-490, 538-624.
GO: GO: 0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                               Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
NCBI TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:virtal envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR000328; Env GP41.

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120; 1.

Pfam; PF00517; GP41; 1.

AIDS; Envelope protein; Transmembrane.
                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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QGUYP4;
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 32; Conservative
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                                                                  PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004; Kuhmann S.B., Pugach P., Kunsteman K.J., Taylor J., Stanfield R.L., Kuster A., Strizki J.M., Riley J. Baroudy B.M., Wilson I.A., Korber B.T., Wolinsky S.M., Moore J.P.; "Generic and phenorypic analyses of human immunodeficiency virus type J. escape from a small-molecule CCRS inhibitor.";
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EMBL, AX357537; AAR00896.1; -; Genomic_DNA.
Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae, Lentivirus, Primate lentivirus group.
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Lentivirus; Primate lentivirus group.
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                                                                                                                                                                                         SMR; QGUYPB; 1-206, 194-491, 539-625. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0013031; C:vixal envelope; IEA. GO; GO:005198; F:structural molecule activity; IEA. InterPro; IPR000328; ENV GP41.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019198; Ferructural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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88.9%; Score 32; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                                                                 EMBL; AY357538; AAR00897.1; -; Genomic_DNA
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AIDS; Envelope protein; Transmembrane.
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QGUYP9;
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NUCLEOTIDE SEQUENCE
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SMR; Q6UYP8; 1-206,
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Kuhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
Korber B.T., Wollntyy S.M., Moore J.P.,
"Genetic and phenotypic analyses of human immunodeficiency virus type
1 escape from a small-molecule CCR5 inhibitor.";
J. Virol. 78:2790-2807(2004).
EMBL: AY357533; AAR00892.1; -; Genomic_DNA.
SMR; QGUYQ3; 1-217, 194-490, 535-624.
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                                                                                                  QGUYQ3;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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641 IYNLLEESQNQQEKNEQELLELDKWANLWWF 672
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Pfam, PF00517, GP41, 1.
AIDS, Envelope protein, Transmembrane.
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InterPro; IPR000777; GP120.
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QGUYQS 9HIV1 PRELIMINARY;
QGUYQS;
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We pubmed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;

We haved=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;

A Kuhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,

A Korhann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,

A Korher B.T., Wolinsky S.M., Moore J.P.,

A Korher B.T., Wolinsky S.M., Moore J.P.,

RT 1 escape from a small-molecule CCRS inhibitor.";

BR 1 escape from a small-molecule CCRS inhibitor.";

BR 2790-2807(2004).

BR 4375529; ARRO8899.1; -; Genomic_DNA.

BR 594904504; 1833.

BR 605 GO:0016021; C:integral to membrane; IEA.

BR 605 GO:0016021; C:integral to membrane; IEA.

BR 605 GO:0018031; C:viral envelope; IEA.

BR 605 GO:0018031; C:viral envelope; IEA.

BR 1 InterPro; IPR000777; GP120.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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E BMBL; AY357530, AAR00890.1; -; Genomic_DNA.

R HSSP; P04578; 1K33.

R SMR; QGUNG; 194-490, 535-624.

R GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:00158; F:structural molecule activity; IEA.

R InterPro; IPR000328; Env GP41.

R InterPro; IPR00077; GP120.

R Ffam; PF00517; GP41; 1.

R AIDS; Envelope protein; Transmembrane.

R NON TER.

I SEQÜENCE 849 AA; 96667 MW; CED40F4AEI574B58 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope glycoprotein (Fragment).
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Pfam; PF00517; GP41; 1.
AIDS; Envelope protein; Transmembrane.
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Sequence 1359,
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Sequence 4
Sequence 4,
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                572060
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/cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                                                                                                                                                                                             YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-515-965A-1358
US-09-515-965A-1359
US-09-350-641C-1358
US-09-350-841A-1359
US-09-350-841A-1359
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                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                             572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                             OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                             US-09-809-060A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                               March
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                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                              Word size :
                                                             OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                             Sequence:
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                                                                                               Run on:
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No.
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4, Appli 1422, Ap 1422, Apl 1422, Apl 143, Appli 18, Appli 19, Appli			Gaps
Sequence Seq			60
Depth		HIV .	36; 18
		н 6	Length Indel
7 5 5 7 4 3		1.25	0
66A-4 48A-14 48A-14 41-4 41-4 41-4 41-4 41-4 41-4 41-4	တ	HIBI.	DB 1 1e-27
7	MENT	DE INHII	ore 36; D ed. No. 1e Mismatches
S-08-487-266A-4 S-09-623-546A-14 S-10-623-546A-14 S-09-657-276-142 S-08-560-921-18 S-08-560-921-18 S-08-955-021-18 S-08-955-021-18 S-08-955-021-18 S-08-073-028-3 S-08-350-817A-15 S-08-484-2238-3 S-08-484-2238-3	ALIGNMENT	128 . PEPTIDE INHIBITORS .ION Americas #1.0, Version #1.25 .73,028	Score Pred.
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0000000000000000000		//080 Dani Donal D	
887333999999999999999999999999999999999		T. 1 -073-028-4 -073-028-4 -073-028-4 No. 5464933 NERAL INFORMATION: APPLICANT: Bolognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Matthews, Thomas J. APPLICANT: Matthews, Thomas J. APPLICANT: Matthews, Thomas J. APPLICANT: Matthews, TRANSMISS NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS: 74 CORRESPONDENCE ADDRESS: 74 CITY: New York STATE: New York STATE: New York CONDUTRY: USA ZIP: 10036 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: EN PC COMPATIBLE COMPUTER: PER PC COMPATIBLE COMPUTER: PER PC COMPATIBLE COMPUTER: PER PC COMPATIBLE COMPUTER: PAPLICATION DATA: MEDILATION NUMBER: 30,742 REGISTRATION NUMBER: 30,742 REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 30,74	66141 PENNIE CHARACTERISTICS: 36 amino acids amino acid amino acid swino acid types: single X: unknown TYPE: peptide 4 100.0% imilarity 100.0%
		cation: 3 3.100:	PENNIE O ID NO FERISTI Lino ac: Cid Engle Bingle Deptide ty 1(
000000000000000000000000000000000000000		Application U 5464933 FORMATION: TT. BAJOUNES, TT. MATCHEWS, TT. MATCHEWS, TT. MATCHEWS, TT. MATCHEWS, TT. MATCHEWS, TT. MATCHEWS, TT. WALCHEWS, TOWN YORK New York New York TYPE: FLOPPY FEE: TEM PC CO- TATION UMBER: TATION NUMBER: THOUGHS PATCHING SYSTEM: TATION SYSTEM: TOWN YORK ATTION NUMBER: TOWN STATION NUMBER	5 G G G G G
1000 1000 1000 1000 1000 1000 1000 100	•	1-4 Applic 5-464933 TERRADATI TERRADATI TERRADATI TERRADATI TO INVENT TO INV	66141 V FOR S CHARAC 36 a amino SDNESS: YYE: 4 YYE: 4
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·		USEOULT 1 USEOB-073-028-4 USEOBLOTA-10-15 SEQUENCE 4, APPLICATION USEDBREAL INPORMATION: APPLICANT: BOLOGNES, APPLICANT: MAICHEWS, APPLICANT: MAICHEWS, APPLICANT: MAICHEWS, APPLICANT: WIGH CARL TITLE OF INVENTION: TOWN YORK COUNTRY: USA ZIP: 1155 Avenue CONFUTER: New YORK STATE: New YORK COMPUTER READABLE FORM MEDIUM TYPE: FLOPPY CONPUTER READABLE FORM MEDIUM TYPE: FLOPPY CONPUTER READABLE FORM MEDIUM TYPE: PATENTIN SOFTWARE: PATENTIN SOFTWARE: PATENTIN SOFTWARE: PATENTIN STATESCOMMUNICATION NUMBER: REGISSTRATION NUMBER: REGISSTRATION NUMBER: REGISSTRATION NUMBER: REFERENCE/DOCKET NUM TELECOMMUNICATION INFORMATION NUMBER: REGISSTRATION INFORMATION NUMBER: REFERENCE/DOCKET NUM TELECOMMUNICATION INFORMATION INFORMA	TELEX: 6614. TELEX: 6614. SEQUENCE CHARAL LENGTH: 36. TYPE: amino STRANDEDNESS TOPOLOGY: un MOLECULE TYPE: 08-073-028-4 uery Match est Local Simila: atches 36: Con
222 222 232 232 244 244 244 244 244 244		SULT 1 Sequence Sequence Patent N GENERAL APPLII APPLII APPLII TITLE TITLE NUMBES COURS STR STR STR STR COU COUN KED COM ATTOR	56 57 d
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ADDRESSEE: Pennie & Edmonds
STREEF: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08484223B
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Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                              149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 36 amino acids TYPE: amino acid
TITLE OF INVENTION: METITILE OF INVENTION: OF TRAINUMBER OF SEQUENCES: 141 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-484-223B-4
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100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels
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ZIP: 10036-211

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-UW-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: COLUZA!, Laura A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUN
   1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                   APPLICANT: Balognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T. APPLICANT: Barney, Shawn O. APPLICANT: Barney, Stephen R. APPLICANT: Petteway, Stephen R. APPLICANT: Langlois, Alphonse J. TITLE OF INVENTION: MEMBRANE FUST TITLE OF INVENTION: B VIRUS TRANS
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Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
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Patent No. 6013263
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Matthews, Thomas J.
Wild, Carl T.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
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MOLECULE TYPE: peptide
US-08-486-099-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
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APPLICANT:
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APPLICANT:
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                                                                                             RESULT 2
US-08-486-099-4
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METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
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APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphones M.
APPLICANT: Langlois, Alphones TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                             CUMPRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUW TYPE: FIDDPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUIA A.
REGISTRENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Gapa

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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: EUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
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                                                                                                                                                                                                                         Length 36;
                                                                                                                                                                                                                                                                  Indels
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
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100.0%; Pred. No. 1e-27;
tive 0; Mismatches 0
                                                                                                                                                                                                                       Score 36; DB 2;
Pred. No. 1e-27;
                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1e-
Matches 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS FOR TITLE OF INVENTION: TRANSMISSION NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08475668A Patent No. 6060065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAULE A.
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : (212) 790-9090
(212) 869-9741/8864
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Matches 36, Conservative
                                                                        36 amino acide
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                             SEQUENCE CHARACTERISTICS
                                                                                                                                   ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-919-597-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                        STRANDEDNESS
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    TELEX:
INFORMATION
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                                                                                            TYPE:
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FRNION: METHODS AND COMPOSITIONS FOR INHIBITION
ENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
FENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2711
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36;
Pred. No. 1
                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
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APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-UN-1995
ATONNEY/AGENT INFORMATION:
NAME: COTUZZI, LBURA A.
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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Patent No. 6054265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambert, Dennis M.
Petteway, Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : (212) 790-9090
(212) 869-9741/8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0%;
Matches 36; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shawn O.
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-484-223B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WILD CARAPPLICANT: Barney, SI APPLICANT: Lambert, APPLICANT: Petteway, APPLICANT: Langlois, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
: New York
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APPLICANT: Bologn
APPLICANT: Matthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                        CLASSIFICATION:
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RESULT 5 US-08-919-597-4

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CITY: STATE:

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MOLECULE TYPE: peptide
NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                             COUNTRY: USA
                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
NUVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
NUVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                  Sequence 4. Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lamglois, Alphones J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
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100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Batentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/485,551A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAMM: COPILEZ, LUMBER: 7872-023

REFERENCE/DOCKET NUMBER: 7872-023

TELEPROCM/MICATION INFORMATION:

TELEPRACE (212) 790-9090

TELEFEX: 6644 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LUMGTH: 36 amino acids

LUMGTH: 36 amino acids

LUMPTH: 36 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                          E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Belognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
APPLICANT: Mild, Carl T.
APPLICANT: Mild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS F.
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                   US-08-485-551A-4
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US-08-471-913A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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Gape
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 74
ADDRESSEE: ADDRESSE:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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ZIP: 10036
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,616
FILING PATE: 06-NOV-1995
FILING PATE: 06-NOV-1995
                                                                                                         CUDNIKK: USA

ZIP: 1038-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elb PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZ, Laura A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REJERPACE (212) 790-9090
TELEFPAC: (212) 790-9090
TELEFPAC: (212) 790-9090
TELEFPAC: (212) 790-9741/8864
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                       1155 Avenue of the Americas
Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08554616
Patent No. 6133418
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TELEPAX: (6141 PENNIE
TELEX: 66141 PENNIE
NPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
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Gaps
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                                                     Length 36;
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100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Merutka, Gene
APPLICANT: Lambert, Dennis
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REPERENCE: 7872-043
FURENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
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APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DAOS: 1515
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                            1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWWF 36
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                                                                                                                                             1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                   100.0%; Score 36; DB 2; 100.0%; Pred. No. 1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 36; DB 2; Best Local Similarity 100.0%; Pred. No. 1e-27; Matches 36; Conservative 0; Mismatches 0
                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FagtSEQ for Windows Version 3.0 SEQ ID NO 1358
LENGTH: 36
                                                                                                                                                                                                                                                                                                      Sequence 1358, Application US/09082279B Patent No. 6258782 GENERAL INFORMATION:
APPLICANT: Barney, Shawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1359, Application US/09082279B Patent No. 6258782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Core polypeptide US-09-082-279B-1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Core polypeptide US-09-082-2798-1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM; Artificial Sequence
                                                   Query Match
Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barney, Shawn
Guthrie, Kelly
Merutka, Gene
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US-09-082-279B-1359
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SEQ ID NO 1359
LENGTH: 36
    US-08-485-264A-4
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Stephen R.
APPLICANT: Lambert, Stephen R.
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
HAPLICATION DATA:
TING DATE: 0.-UUN-1995
FILING DATE: 0.-UUN-1995
FILING DATE: 0.-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                   NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCET DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: gridle
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1155 Avenue of the Americas
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CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: COTUZAL, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08485264A Patent No. 6228983 GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 36 amino acide
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-485-264A-4
                                                                                                                                                                                                                                                                                                                                                       US-08-554-616-4
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US-09-315-304B-1359
; Sequence 1359, Application US/09315304B
; Patent No. 6348568
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CTHER INFORMATION: Core polypeptide

US-09-315-3048-1358
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                                                                                                                                               Sequence 4, Application US/08474349A

Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Stephen R.

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100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZi, Laura A.
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
                                            1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1358, Application US/09315304B
Patent No. 6488568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Macuthia, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-474-349A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYEPTIDES WITH ENHANCED PHARMACCKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FeatSEQ for Windows Version 3.0
SEQ ID NO 1359
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APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: PSASESEQ for Windows Version 3.0
SEQ ID NO 1358
LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 36; DB 2; Best Local Similarity 100.0%; Pred. No. 1e-27; Matches 36; Conservative 0; Mismatches 0
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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protein search, using sw model OM protein

Run on:

US-09-809-060A-3 36 Title:

1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36 Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

1867569 seqs, 417829326 residues Searched:

0 Word size :

Total number of hits satisfying chosen parameters:

1867569

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA Main:*

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Sequence 13, Appl Sequence 11, Appl Sequence 28, Appl Sequence 30, Appl Sequence 31, Appl Sequence 11, Appl Sequence 11, Appl Sequence 1082, Ap Sequence 1083, Ap	73; 125; 72; 124; 635; 60;
US-11-018-102-13 US-09-131-551-11 US-09-854-816-28 US-09-854-816-30 US-09-854-816-31 US-11-018-102-11 US-11-0351-641-1082 US-10-351-641-1083 US-10-005-305-58	US-10-005-305-73 US-10-950-010-125 US-10-005-305-59 US-10-005-305-72 US-10-950-010-124 US-10-351-641-635 US-10-351-641-637 US-10-005-305-60
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145 145 145 269 269 21 21	. 299 88 27 29 29 29 29 29 29 29 29 29 29 29 29 29
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9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	8 6 6 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6

ALIGNMENTS

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APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 36
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Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-3
Sequence 3, Application US/09809060 Publication No. US20020010317A1 GENERAL INFORMATION:
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1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36

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US-10-252-136-4

Sequence 4, Application US/10252136;
Sequence 4, Application US/10252136;
Publication No. US20030103998A1
GENERAL INFORMATION:
APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNOBEFICIENCY VIRUS AND OTHER
TITLE OF INVENTION: USING COMBINATORY THERAPY
TITLE OP INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 7872-036
CURRENT FILING DATE: 2002-09-20
PRIOR PILING DATE: 2002-09-20
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4

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ORGANISM: Artificial Sequence
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                               FEATURE:
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APPLICANT: Barney, S.
APPLICANT: Barney, S.
APPLICANT: Barney, S.
APPLICANT: Merutka, G.
APPLICANT: Merutka, G.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT PRILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,041
PRIOR PILING DATE: 1999-05-20
PRIOR PAPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastESQ for Windows Version 3.0
SEQ ID NO 1358
LEGGET: 36
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APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPRENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT PILING DATE: 2003-01-24
PRIOR PRILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
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                                                                                                                         Query Match
100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels
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100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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                                                ; ORGANISM: Human immunodeficiency virus US-10-252-136-4
                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1358, Application US/10351641; Publication No. US20030186874A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1359, Application US/10351641 Publication No. US20030186874A1 GENERAL INFORMATION:
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APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
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LENGTH: 36
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MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                      1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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100.0%; Pred. No. 9e-28;
tive 0; Mismatches 0
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CLASSIFICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAMM: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1155 Avenue of the Americas CITY: New York
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SEQ TO NO 1359
LENGTH: 36
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TOPOLOGY: unknown
WOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
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                                                                                                                                                                                                                 OTHER INFORMATION: Core polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Lambert, Dennis M.
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RESULT 9
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                                               Gaps
Query Match
100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <UNknown>
                                                                                         1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-9741/8864
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Langlois, Alphonse
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TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                Sequence 4, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
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MEDIUM TYPE: Floppy disk
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Best Local Similarity
Matches 36; Conserva
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RESULT

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Sequence 39, Application US/10671282
Publication No. US20040122214A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and TITLE OF INVENTION: their use in therapy
FILE REPERENCE: TRM-00A.
CURRENT APPLICATION NUMBER: US/10/671,282
PRIOR PAPLICATION NUMBER: 60/414,439
PRIOR PAPLICATION NUMBER: 60/414,439
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 114
SSCPTWARE: Patentin version 3.2
SSCPTWARE: Patentin version 3.2
SSCPTWARE: Patentin version 3.2
                                                                                                 TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV IITLE OF INVENTION: gp41-derived peptides, and its use in therapy FILE REFERENCE: TRM-003
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Publication No. US20050065319A1
GENERAL INFORMATION:
APPLICANT: Baroudy, Bahige M.
TITLE OF INVENTION: Combination Method For Treating Viral Infections
FILE REPRENENT: 1001358
CURRENT APPLICATION NUMBER: US/10/168,295
CURRENT FILING DATE: 2002-06-19
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Pred. No. 9e-28;
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Pred. No. 9e-28;
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Best Local Similarity 100.0%; Pred. No. 9e-
Matches 36; Conservative 0; Mismatches
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100.0%; Score 36; DE
Best Local Similarity 100.0%; Pred. No. 9e-
Matches 36; Conservative 0; Mismatches
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US.60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2
SEQ ID NO 39
LENGTH: 36
Sequence 39, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
COTHER INFORMATION: Synthesized
US-10-671-282-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthesized
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                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial
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TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500662002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR PLING DATE: 1099-09-07
PRIOR PLING DATE: 1099-10
PRIOR PILING DATE: 1999-10
PRIOR PILING DATE: 1999-10
PRIOR PILING DATE: 1999-10
PRIOR PILING DATE: 1999-1015
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PALECATION VUMBER: 60/159,783
PRIOR PALLOR DATE: 1999-1015
NUMBER OF SEQ ID NOS: 1617
SEQ ID NO 1422
LENGTH: 36
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TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: Peptide US-11-066-697-1422
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OFERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRITAN APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: CUNKNOWN>
APPLICATION WIMBER: 08/965,056
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION: CUNKNOWN>
ATTORNEY/AGENT INFORMATION: CUNKNOWN>
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REFERENCE/DOCKET NUMBER: P1005R2
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J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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ORGANISM: Artificial Sequence
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APPLICANT: BULDON, Dominique P.
APPLICANT: BULDON, Dominique P.
APPLICANT: BULDON, Nissab
APPLICANT: BOBITAILLE, Martin
APPLICANT: MILNER, Peter G.
ITITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
ITITLE OF INVENTION: INPECTION
FILE REFERENCE: 500862001501/REDC-1512
CURRENT APPLICATION NUMBER: US/10/950,010
FURRENT APPLICATION NUMBER: US 09/623,533
PRIOR PILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-05-17
PRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 545
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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US-10-950-010-4
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100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels
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100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                ; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-4
PRIOR APPLICATION NUMBER: PCT/US01/48802
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,657
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 62
SOFUMARE: Patentin version 3.1
ENGITH: 36
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Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Bridon, Dominique P.
APPLICANT: Bridon, Paren G.
APPLICANT: Milner, Peter G.
APPLICANT: Holfes, Earfen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10950010; Publication No. US20050070475A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-11-066-697-1422
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LENGTH: 36
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OTHER INFORMATION: Synthetic Peptide corresponding to gp41 amino OTHER INFORMATION: acids 131 - 175
                                                                                                APPLICANT: Wray, Larry K.
APPLICANT: Falk, Lawrence A.
APPLICANT: Pavare, Sushil G.
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODY (5-21-3) TO
TITLE OF INVENTION: HUMAN IMMUNOBERICIENCY VIRUS GP41 PROTEIN
FILE REPERBNCE: 4573.US.C6
                                                                                                                                                                                                                                                                                  CURRENT PELICATION NUMBER: US/10/086,409A
CURRENT FILING DATE: 2001-11-19
PRIOR PELING DATE: 1997-06-14
PRIOR FILING DATE: 1997-06-14
PRIOR FILING DATE: 1995-12-27
PRIOR FILING DATE: 1995-12-27
PRIOR FILING DATE: 1995-01-23
PRIOR FELLORITON NUMBER: 08/376,694
PRIOR FILING DATE: 1995-01-23
PRIOR FILING DATE: 1991-06-02
PRIOR FILING DATE: 1991-10-22
PRIOR FILING DATE: 1991-10-22
PRIOR FILING DATE: 1991-10-22
PRIOR FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FEALSEQ FOR WINDOWS VERSION 4.0
SOFTWARE: FEALSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 EESQNQQEKNEQELLELDKWANLWNW 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                       Dawson, George J.
Sarin, Virender K.
                                                                                             Webber, J. Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.2
Best Local Similarity 100.
Matches 26; Conservative
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Dawson, George J.
APPLICANT: Basin, Virender K.
APPLICANT: Webber, J. Scott
APPLICANT: Webber, J. Scott
APPLICANT: Webber, J. Scott
APPLICANT: Weay. Larry K.
APPLICANT: Wray. Larry K.
CURRENT APPLICATION NUMBER: US/10/086,409A
PRIOR PILING DATE: 1995-01-23
PRIOR APPLICATION NUMBER: 08/579,088
PRIOR PILING DATE: 1995-01-23
PRIOR APPLICATION NUMBER: 08/101,082
PRIOR PILING DATE: 1995-01-23
PRIOR APPLICATION NUMBER: 07/766,576
PRIOR APPLICATION NUMBER: 07/766,576
PRIOR APPLICATION NUMBER: 07/776,077
PRIOR APPLICATION NUMBER: 08/50-30-30
NUMBER OF SEQ ID NO 3
LENGTH: 38
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                                                                                                                                                                                                                                                                                                                                                                                      169 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNF 204
                                                                                                                                                                                                                                                                                                                                                     1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
                                                                                                                  TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10086409A Publication No. US20030118985A1 GENERAL INFORMATION:
                                                      LENGTH: 269 amino acids
TYPE: Amino Acid
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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US-10-086-409A-3
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72.2%; Score 26; DB 4; Length 45; 100.0%; Pred. No. 5.7e-18; tive 0; Mismatches 0; Indels

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Sequence 2, Application US/09809060;
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: Neutralizing Ancibodies against Fusion-Active;
TITLE OF INVENTION: Negions of HIV Envelope Proteins
FILE REFERENCE: 1900.026001;
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 2.
LENGTH: 36
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APPLICANT: Abbott Laboratories

8 LLEESQNQQEKNEQELLELDKWA 30

Search completed: March 6, 2006, 16:32:48 Job time: 97.3333 secs

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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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STRANDEDNESS: <Unknown>
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US-11-084-858-11
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                                                                            March 6, 2006, 16:28:08; Search time 10.3333 Seconds (without alignments) 69.679 Million cell updates/sec
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Sequence 4,
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// CGRZ 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
// CGRZ 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
// CGRZ 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
// CGRZ 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
// CGRZ 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
// CGRZ 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
// CGRZ 6/ptodata/2/pubpaa/US11 NEW PUB.pep:*
// CGRZ 6/ptodata/2/pubpaa/US11 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                           1 YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF 36
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US-11-029-003-1
US-11-112-277-33
US-11-112-277-33
US-11-187-687-24
US-10-841-956A-8
US-10-841-956A-8
US-10-841-956A-9
US-10-841-956A-9
US-10-841-956A-9
US-10-841-956A-9
US-10-841-956A-9
US-10-841-956A-9
US-11-053-100-37
US-11-053-100-33
US-11-053-100-33
US-11-053-100-33
US-11-053-100-33
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                                                                                                                                                                                                                            135346 segs, 20000420 residues
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                                                   OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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US-10-506-796A-1
US-11-151-598-4
US-11-151-598-4
US-10-506-796A-9
US-11-151-598-1
                                                                US-11-112-277-36
                                                                            US-11-151-598-12
                                               US-11-151-598-9
US-11-151-598-2
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ALIGNMENTS

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AFFLICTION KNAPP, Stefan
GERKEN, Manfred
GUERTLER, Lutz
TITLE OF INVENTION: Peptides derived from a retrovirus of
the HIV group, and their use
                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/084,858
FILING DATE: 21-Mar-2005
CLASSIPTCATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/000,321
FILING DATE: 04-Dec-2001
APPLICATION NUMBER: 09/131,551
FILING DATE: CURROWN-
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
AREFERENCE/DOCKET NUMBER: 58315/106/BEAK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington
Sequence 11, Application US/11084858
Publication No. US20080271678A1
GENERAL INFORMATION:
APPLICANT: BRUST, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
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FEATURE:
NAME/KEY: MOD_RES
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Sequence 1, Application WS/11029003

Publication No. US20050260194A1

GENERAL INFORMATION:
APPLICANT: BTORN, DANIEL S.
APPLICANT: BTORN, DANIEL S.
APPLICANT: BTORNI, ALM J.
APPLICANT: STATEL, JAMES

TITLE OF INVENTION: IMMUNOGIOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
FILE REPERENCE: 08945.0007-01000

CURRENT APPLICATION NUMBER: US/11/029,003

CURRENT FILING DATE: 2005-01-26
PRIOR APPLICATION NUMBER: 60/487,964

PRIOR PILING DATE: 2003-07-17

PRIOR PILING DATE: 2003-07-17

PRIOR PILING DATE: 2003-05-06

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PATCHING DATE: 2003-05-06

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PATCHING DATE: 2003-05-06

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PATCHING DATE: 2003-05-06

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PATCHING DATE: 2003-05-06

NUMBER OF SEQ ID NOS: 91

SEQ ID NO I BLOOK DATE: 2003-05-06
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Sequence 1, Application US/10841956A

Publication No. US2050281829A1

GENERAL INFORMATION:

APPLICANT: TAN HEHIR, CRISTINA A.

APPLICANT: PETERS, ROBERT T.

APPLICANT: PETERS, ROBERT T.

APPLICANT: PITEL, JAMES M.

APPLICANT: PITONTI, ALAN R.

TILLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS

FILE REPERENCE: 08945-0003-00000

CURRENT APPLICATION NUMBER: US/10/841,956A

CURRENT APPLICATION NUMBER: 60/468,835

PRIOR APPLICATION NUMBER: 60/468,835

PRIOR APPLICATION NUMBER: 60/468,835

SOFTWARE: PATENT OF THE STATE STAT
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                                                                               Query Match 63.9%; Score 23; DB 7; Length 145; Best Local Similarity 100.0%; Pred. No. 9.6e-17; Matches 23; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-029-003-1
                                                                                                                                                                                                                                                                                                            8 LLEESQNQOEKNEQELLELDKWA 30
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US-11-084-858-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-841-956A-1
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APPLICANT: Intecout, ALCY E.
APPLICANT: Litzinger, David C.
APPLICANT: Kimmel, Bruce E.
APPLICANT: Kimmel, Bruce E.
APPLICANT: Kimmel, Bruce E.
APPLICANT: Kimmel, Bruce E.
TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino TITLE OF INVENTION: Acids
TITLE OF INVENTION: Acids
FILE REPERBRICE: AMBX-0041.00US
CURRENT APPLICATION NUMBER: 00/590,035
PRIOR PILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: 60/590,035
PRIOR APPLICATION NUMBER: 60/590,035
PRIOR APPLICATION NUMBER: 60/590,035
PRIOR PILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 36
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Query Match 58.3%; Score 21; DB 7; Length 36; Best Local Similarity 100.0%; Pred. No. 2.7e-15; Matches 21; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.7e-15;
tive 0; Mismatches 0;
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; ORGANISM: Human immunodeficiency virus
US-11-187-687-22
                                                                                                                                                                                                                                                                                 Sequence 22, Application US/11187687; Sequence 22, Application US/11187687; Publication No. US20060019347A1; GENERAL INFORMATION: APPLICANT: Cho, Ho Sung APPLICANT: Haye, Anna-Maria APPLICANT: Haye, Anna-Maria APPLICANT: Wilson, Troy E.
                                                                                                        10 EESONOOEKNEGELLELDKWA 30
                                                                                                                                               10 EESQNQQEKNEQELLELDKWA 30
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Sequence 33, Application US/11112277
Publication No. US20050267293A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 21; Conservative
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PEATURE: Peptide
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
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; Sequence 8, Application No. US2050281829A1
; Publication No. US20650281829A1
; GENERAL INFORMATION:
    APPLICANT: TAN HEHIR, CRISTINA A.
    APPLICANT: PETERS, ROBERT T.
    APPLICANT: PATATEL, JAMBS M.
    APPLICANT: BALOMBELLA, VITO J.
    APPLICANT: BITONII, ALAN R.
    APPLICANT: BITONII, ALAN R.
    FILE REFERENCE: 08945.0003-000000
    CURRENT APPLICATION UNDRER: US/10/841,956A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TAN HEHIR, CRISTINA A.
APPLICANT: MEZO, ADAM R.
APPLICANT: PETERS, ROBERT T.
APPLICANT: STATTEL, JAMES M.
APPLICANT: PALOMBELLA, VITO J.
APPLICANT: BITONTI, ALAN R.
TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945.0003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT FILING DATE: 2004-05-06
                                                                                                                                                                DB 7; Length 44; 3.3e-15;
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                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 3.3
Matches 21; Conservative 0; Mismatches
                                                            TYPE: PRT / ORGANISM: Human immunodeficiency virus US-11-187-687-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 4
LENGTH: 267
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PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 8
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    SOFTWARE: Patentin version 3.3
SEQ ID NO 24
LENGTH: 44
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APPLICANT: Cho, Ho Sung
APPLICANT: Daniel, Thomas O.
APPLICANT: Daniel, Thomas O.
APPLICANT: Hays, Anna-Maria
APPLICANT: Hays, Anna-Maria
APPLICANT: Litzinger, David C.
APPLICANT: Mariani, Roberco
APPLICANT: Acide
APPLICANT: Refer, William M.
TITLE OF INVENTON: Bosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
TITLE OF INVENTON: Acide
FILE REFERENCE: AMBX-0041.00US
CURRENT FILING DATE: 2005-07-21
PRIOR FILING DATE: 2004-07-21
PRIOR FILING DATE: 2004-07-21
PRIOR FILING DATE: 2005-03-07
PRIOR FILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%; Score 21; DB 7; Length 44; 100.0%; Pred. No. 3.3e-15; ive 0; Mismatches 0; Indels
                                                                                            Query Match 58.3%; Score 21; DB 7; Length 37; Best Local Similarity 100.0%; Pred. No. 2.8e-15; Matches 21; Conservative 0; Mismatches 0; Indels
; LOCATION: 37; CTHER INFORMATION: Xaa is Lys linked to AEEA-MPA US-11-112-277-33
                                                                                                                                                                                                                                                                                                         RESULT 6
US-11-089-426-10
; Sequence 10, Application US/11089426
; Publication No. US20050261229A1
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Publication No. US20060019347A1
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SEQ ID NO 7
LENGTH: 281
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Peptide
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nes 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: Peptide
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Matches
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                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: CONStruct
US-10-841-956A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: Peptide
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MEZO, ADAM R.
APPLICANT: PETERS, ROBERT T.
APPLICANT: STATTEL, JAMES M.
APPLICANT: STATTEL, JAMES M.
APPLICANT: BITONII, ALAN R.
TILLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
FILE REFERENCE: 08945.0003-000000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT FILING DATE: 2004-05-06
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOFFWARE: PATENTIN VET. 3.2
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APPLICANT: PETERS, ROBER. T.
APPLICANT: PETERS, ROBER. T.
APPLICANT: PALOMBELLA, VITO J.
APPLICANT: PALOMBELLA, VITO J.
APPLICANT: PALOMBELLA, VITO J.
APPLICANT: PALOMERIA, VITO J.
APPLICANT: APPLICANTON R.
FILE REFERENCE: 08945.0003-00000
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS. 59
SOFTWARE: PALENTIN VET. 43.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 270;
                                                                                                                                                           Score 21; DB 6; Length 269
Pred. No. 1.9e-14;
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Pred. No. 1.9e-14;
                                                                                                                                                                                                0; Indels
                                                                                                                                           58.3%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/10841956A; Publication No. US20050281829A1; GENERAL INFORMATION: APPLICANT: TAN HEHIR, CRISTINA A. APPLICANT: MEZO, ADAM R. APPLICANT: PETERS, ROBERT T.
                                                                                                                                                                                                                                       10 EESQNQQEKNEQELLELDKWA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 EESQNQQEKNEQELLELDKWA 30
                                    ORGANISM: Artificial Sequence
FEATURE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 5
LENGTH: 270
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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Best Local Similarity 100.0
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                       US-10-841-956A-5
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: construct
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APPLICANT: PETERS, ROBERT T.
APPLICANT: PETERS, ROBERT T.
APPLICANT: PETTEL, JAMES M.
APPLICANT: PALOMBELLA, VITO J.
APPLICANT: BITONII, ALAN R.
TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945.0003-000000
CURRENT APPLICATION NUMBER: 05/10/841,956A
CURRENT PILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PALENTIN Ver. 3.2
LENGTH: 282
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APPLICANT: PETERS, ROBERT T.
APPLICANT: STATTEL, JAMES M.
APPLICANT: STATTEL, JAMES M.
APPLICANT: BITONII, ALAN R.
TILLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945, 0003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR APPLICATION NUMBER: 60/468,835
NUMBER OF SEQ ID NOS: 59
                                                                                                 58.3%; Score 21; DB 6; Length 281;
100.0%; Pred. No. 2e-14;
tive 0; Mismatches 0; Indels
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Pred. No. 2e-14;
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; Publication No. US20050281829A1
; GENERAL INFORMATION:
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Publication No. US20050281829A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                        Best Local Similarity 100.
Matches 21; Conservative
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Publication No. US2005025554A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION FUSION PERTIDES ISOLATABLE BY PHASE TRANSITION
TITLE OF INVENTION: FUSION PERTIDES
CURRENT APPLICATION UNMBER: US/11/053,100

CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 09/812,382
PRIOR APPLICATION NUMBER: US 09/812,382
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
SOFTWARE: Patentin version 3.3
SEQ ID NO 27

LENGTH: 354
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; Sequence 36, Application US/11053100
; Publication No US2005025554A1
; GENERAL INFORMATION:
    APPLICANT: CHILKOTI, Ashutcsh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; TITLE OF INVENTION: US/11/053,100
; CURRENT APPLICATION NUMBER: US/11/053,100
; CURRENT FILING DATE: 2005-02-08
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2000-03-20
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Version 3.3
; SEQ ID NO 36
                                                                                                                             FEATURE: Peptide
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
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; OTHER INFORMATION: pET15b-ELP4-60-EK-T20 peptide
US-11-053-100-27
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OTHER INFORMATION: Synthetic Construct
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                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 9
LENGTH: 293
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ORGANISM: Artificial
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US-11-053-100-36
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TYPE: PRT

ORGANISM: Artificial
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CTHER INFORMATION: Synthetic Construct
FEATURE:
COTHER INFORMATION: Synthetic Construct
FEATURE:
COTHER INFORMATION: FEATURE
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BEST Local Similarity 100.0%; Pred. No. 2.5e-14;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;

MATCHES 21; CONSERVATION: 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 EESONQOEKNEQELLELDKWA 30

Db 330 EESONQOEKNEQELLELDKWA 350

Search completed: March 6, 2006, 16:33:25
Job time: 10.3333 secs
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DP178-lik Hybrid po HIV gp41 Transmemb

HIV-1 gp4 Core poly Viral DP1 Viral cor DP178-lik

Core poly Core poly Viral DP1 DP178-lik Hybrid po

DP178 hom

HIV-1 gp4 Core poly

Per Viral

Abol0166
Aay89911
Aaby89312
Abb01319
Ada013865
Ada02215
Abb00638
Ada021186
Ada021186
Ada021353
Ada021353
Ada02033
Ada0639
Ada06039
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Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon;
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                                                                                                                                                                                                      ALIGNMENTS
                                                   ADE02837
ADU80515
ADZ40273
AAB77633
                                                                                                              ADE02135
ADG13553
ADU80509
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                         AAB78312
ABB01319
                                                                                     ABB02115
ABB00638
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ABB00639
                                           4AU13865
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                                                                                                                                                                                                                                                                                  (first entry
                 WO9959615-A1.
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137.945 Million cell updates/sec
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                                                            6, 2006, 15:31:26 ; Search time 114.667 Seconds
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                              1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF
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Maximum Match 100%
Listing first 45 summaries
                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (1941) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or function of a disease. The core polypeptides are bloactive peptides selected from a growth factor, cytokine, differentiation factor, or selected from a growth factor, cytokine, differentiation factor, not neglogenic interleukin, interferon, colony stimulating factor, hormone or anglogenic A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence. Disclosure; Page 45; 124pp; English. WPI; 2000-136792/12

Viral cor DP178-lik DP178-lik HIV 9P41 HIV 9P41 HYbrid po HYbrid po

Aau13795 Aao18774

AAU13794 AAU13795 AAO18774 AAO18826

ABB01248 ABB01249

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100.

AAB78242 AAB78241

Score

Result

ADE02854 ADE02853 ADN06925 ADS87260

Peptide c DP-178-li HIV antiv

rel gp4

Virus HIV-1

Aab54788 H Aab92247 N Aag67042 H

AAG67042

COL

Viral

Aar98401

ABB02834 AAR98401 ADY71495

Ade02854 F Ade02854 F Ade02853 F Adn06925 Ads87260 F Ady71547 F Ady71495 F Abb02834 V

Lambert DM;

Anwer MK,

Merutka G,

Barney S, Guthrie KI, (TRIM-) TRIMERIS INC

98US-00082279

20-MAY-1998;

Core poly Core poly Core poly poly poly Core poly HIV viral

Aay89840

Viral

Aab78241

Abb01248 Abb01249 Abb02833 Aau13794

Pred. No. 2.1e-16;

Similarity

Best Local

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The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gg41) protein sequences, especially from HIV-1, HIV-2 and SIU. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any colypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or prevention of a disease. The core polypeptide for the treatment or prevention of a disease. The core polypeptide are bloactive peptides selected from a growth factor, cytokine, differentiation factor, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used in anti-fusogenic treatments. Sequences AAY88651-Y80055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also
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             infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; angiogenic factor.
 The peptides of the invention can be used for inhibiting viral
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                                                                                                                                                     Length 36;
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                                                                                                                                                     100.0%; Score 192; DB 3; 100.0%; Pred. No. 2.1e-16;
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                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 45; 124pp; English.
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                                                                                                                                                                                                                                                                                                                                                                AAY89841 standard; peptide; 36
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100.0%; Score 192; DB 3; Length 36;

Query Match

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The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide can be used to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide can be used for modulating fusogenic events and intracellular processes involving coiled-coil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg fusion) interacellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus. cepiratory syncytial infections caused by human immunodeficiency virus, respiratory syncytial virus, beptein-Barr virus, hepatide sequence increases the half-life and polio virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the increases the sensitivity of the diagnostic
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                                                                                                                                                                                                                                                                                                           Core polypeptide, enhancer, antiviral, anti-HIV, virucide, hepatotropic, antiinflammatory, hybrid polypeptide, coiled-coil peptide interaction, fusion-related disorder; bacterial infection, viral infection.
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100.0%; Prea. ....
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                                                                                                                                                                           AAB78242 standard; peptide; 36 AA
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                                                                                                                                                                                                                                            (first entry)
                      36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barney S, Guthrie KI,
                                                                                                                                                                                                                                                                           Core polypeptide T1410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-147136/15
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tes 36, Conserv
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                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide.
                                                                                                                                                                                                                                            19-APR-2001
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                                                                                                                                                                                                          AAB78242;
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                    Matches
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(first entry)

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Human, HIV-1, human immunodeficiency virus, gp41; glycoprotein 41; gp120;
anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
alpha-helical region; ectodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic composition for inhibiting HIV infection, comprises viral envelope protein or its fragment exterior to viral membrane, a stabilizing peptide, and, optionally, viral cell surface receptor or its
                                                                                HIV viral envelope protein stabilising peptide #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 45; 84pp; English.
                                                                                                                                                                                                                                                                                                                                    15-MAR-2001; 2001WO-US008108.
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                                                                                                                                                                                                                                                                                                                                                                                                                    (PANA-) PANACOS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-626098/72.
                                                                                                                                                                                                                                                  NO200170262-A2
                                         14-FEB-2002
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wild CT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide and note polypeptides on be used for modulating fusgenic events and intracellular processes involving coiled coil peptide interactions. Other uses include preventing, treating and/or aliagnosing disporders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus, respiratory syncytial cinfections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and creduces the clearance rate of therapeutic peptides, which increases their effects. In addition, this increases the sensitivity of the diagnostic
                                                                                                                                                                                                                                             Core polypeptide, enhancer, antiviral, anti-HIV, virucide, hepatotropic, antiinflammatory, hybrid polypeptide, coiled-coil peptide interaction, fusion-related disorder, bacterial infection, viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lambert DM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 58; 151pp; English.
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                                                                             AAB78241 standard; peptide; 36 AA.
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Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                       Core polypeptide T1409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guthrie KI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TRIM-) TRIMERIS INC.
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                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                      AAB78241;
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                                                          AAB78241
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Allaway GP;

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The invention relates to methods of generating immunogens that elicit neutralising antibodies which target regions of viral envelope proteins such as the gap120/ggl/ (glycoprotein 120/glycoprotein 41) complex of HIV-1 (thuman immunodeficiency virus 1) Sequences AAU70179-AAU70199 and AAU70677-AAU70743 represent stabilising peptides modelling the alphabelical regions of the ectodomain of the HIV-1 transmembrane protein to stabilise fusion-active intermediate structures, which can be used as vaccine immunogens. Immunogenic compositions comprise a viral envelope protein or its fragment exterior to the viral membrane, a stabilising protein or its fragment exterior to the viral membrane, a stabilising viral fusion and entry, and optionally, a viral cell surface receptor or its fragment. The stabilising peptide is capable of associating with the envelope protein or its fragment to form a stabilised, fusion active structure. Antibody binding assays are used to determine the ability of immunogen vaccines to generate an immune response to various forms of envelope. Virus neutralisation assays can be used to characterise the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody response raised against HIV-1 gp41 domains. The sequences and methods are useful for inhibiting HIV infection, for inducing an immune
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100.0%; Pred. No. 2.1e-16;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response in an animal and for raising antibodies
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Best Local Similarity 100.0%;
Matches 36; Conservative 0
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03-JAN-2002
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Gaps

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AAU70182 standard; peptide; 36 AA

AAU70182 ID AAU7 XX RESULT 5

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29-FEB-2000; 2000US-00515965
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ses 36; Conserv
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                                           WO200164013-A2
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06-AUG-2003
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                      Viruses.
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                                                                                                                                                                                                                                                                                                                    Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                              Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus, HIV; respiratory syncytial virus, RSV,
virucide, heptad repeat region, transmembrane protein, gp41, HR1, HR2,
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100.0%; Pred. No. 2.1e-16;
live 0; Mismatches 0;
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          Viral DP178/107-like region peptide T1409
                                                                                                                                          /note= "C-terminal amide"
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                                                                                                Location/Qualifiers
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Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                         Modified-site
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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107 correspond to amino acids 638-637 (heptad repeat region HR2) and 558-558 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-40G-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                              Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
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llarity 100.0%; Pred. No. 2.1e-16;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 58; 587pp; English
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07-FEB-2001; 2001WO-US003988
                                                                    29-FEB-2000; 2000US-00515965
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                                                                                                                                                                                                         Antczak JB, Delmedico MK,
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                                                                                                                                                The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-633 (heptad repeat region HR2) and 558-555 (heptad repeat region HR1) respectively, of HIV-LIAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 0.6-MUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                               Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41; antifusogenic; antiviral; HIV transmission; mutant; mutein.
                                   Sista P;
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                                                                                                                                                                                                                                                                                                                                   Length 36;
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                                   Lambert DM,
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                                                                                                                                                                                                                                                                                                                                 100.0%; Score 192; DB 4; 100.0%; Pred. No. 2.1e-16;
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                                   Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP178-like/DP107-like peptide T-1409.
                                                                                                                             Disclosure; Page 525; 587pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU13794 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2000; 2000WO-US035727
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                                  Delmedico MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                        Conservative
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            (TRIM-) TRIMERIS INC.
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                                                                                                                                                                                                                                                                                                                    WPI; 2001-442157/47.
                                                         WPI; 2001-514829/56
                                                                                                                                                                                                                                                                                                          Sequence 36 AA;
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                                   Antczak JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-2001
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                                                                                                         infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU13794;
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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU1259-AAU1009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate IAI. The DP107 peptide corresponds to amino acids 588-595 of gp41 from HIV-1LAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex. The method comprises absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral.
  or disrupts a
sogenic, antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to peptides which exhibit anti-retroviral
ntifying a compound that inhibits the formation of or disrupts a 0.7/DP178 complex, especially compounds with antifusogenic, antivirs intracellular modulatory activity, by detecting the formation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particularly HIV, transmission to uninfected cells. The present seque: represents one of the DP178-like/DP107-like peptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 192; DB 4; Length 36; Best Local Similarity 100.0%; Pred. No. 2.1e-16; Matches 36; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawless MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 1; isolate LAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DP178-like/DP107-like peptide T-1410.
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                                                                                                                        Disclosure; Page 77; 259pp; English
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                                                                        OP107/DP178 complex,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 AA;
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  Identifying
DP107/DP178
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The present invention relates to a method of treating an HIV infection in an individual, which involves administering in combination a chemokine co-receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its derivative. Other viral infections can also be treated using the method. The present sequence is a peptide derived from HIV and useful in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of HIV infection in an individual involves administration of a combination of chemokine co-receptor five antagonist and a specified HIV
                                                                                                                                                                                                                                                                                                                                                                                         Viral infection, HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
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                                                                                                                                                                                                                                                                                                                                             HIV gp41 protein DP-178 region derived peptide SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 192; DB 5; Local Similarity 100.0%; Pred. No. 2.1e-16; nes 36; Conservative 0; Mismatches 0;
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                                                     1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF
                                                                                             1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF
         Mismatches
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         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             combination of chemok
envelope polypeptide.
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           36;
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                                                                                                                                                                                                                                                         AA018826;
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activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-LLAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like peptides are useful to inhibit human and non-human retroviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method of treating an HIV infection in an individual, which involves administering in combination a chemokine co-receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its derivative. Other viral infections can also be treated using the method. The present sequence is a peptide derived from HIV and useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of HIV infection in an individual involves administration of a combination of chemokine co-receptor five antagonist and a specified HIV envelope polypeptide.
                                                                                                                                                                                                                                                                                                   particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 192; DB 4;
Pred. No. 2.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF
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Best Local Similarity
Matches 36; Conserv
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Best Local Similarity
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Pharmaceutical; human immunodeficiency virus; HIV; gp41; glycoprotein41;
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                                                                                   20-MAY-1999;
                                                                                                              20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                   peptide sequence enhances pharmacokinetic properties of any core polypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging structures in vivo. The core polypeptides and hybrid polypeptides are useful for modulating fusogenic events and exhibit antifusogenic or antivital infection and modulating intracellular processes involving coiledial peptide interactions. The novel hybrid polypeptide comprises insulin or its fragment, so the core polypeptide is useful for ameliorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also useful as a part of prognosis for preventing disorders including fusion events and viral infection that involves cell-cell and/or virus-cell fusion, and for diagnosis and in vivo imaging methods. This sequence
                                                                                                                                                                                                                    New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
                                                                                                                                                                                                                                                                                                     The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WQSWEQKI or WASLWEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel hybrid polypeptide has virucide and antidiabetic activity. The enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion, and for diagnosis and in vivo imaging methods. This sequence represents an enhancer peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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pharmacokinetic; fusogenic; insulin; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Residue is modified by acetyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 192; DB 5; Length 36; 100.0%; Pred. No. 2.1e-16; ive 0; Mismatches 0; Indels
                                                                                                                                                                   Anwer MK, Lambert DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 1361; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                   Merutka G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE02853 standard; peptide; 36 AA
                                                                                   99US-00315304
                                                                                                            98US-00082279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                Guthrie KI,
                                                                                                                                      (TRIM-) TRIMERIS INC
                                                                                                                                                                                             WPI; 2002-424396/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
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Unidentified
                           US6348568-B1
                                                                                 20-MAY-1999;
                                                                                                            20-MAY-1998;
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                                                     19-FEB-2002
                                                                                                                                                                  Barney S,
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The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WGBWEGKI or WASLWEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel bybrid polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core copypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging core structures in vivo. The core polypeptide and hybrid polypeptides are useful for modulating fusogenic events and exhibit antifusogenic or antiviral activity. The novel hybrid polypeptide is useful for decreasing coll peptide interactions. The novel hybrid polypeptide comprises insulin or its fragment, so the core polypeptide is useful for anellorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also custing as a part of prognosis for preventing disorders including fusion events and viral infection that involves cell-cell and/or virus-cell fusion, and for diagnosis and in vivo imaging methods. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Lambert DM;
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Pred. No. 2.1e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Anwer MK,
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100.0%; Pred. No. ...
0; Mismatches
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/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Merutka G,
                                                                                                                                                                                                                    99US-00315304.
                                                                                                                                                                                                                                                                                            98US-00082279
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Barney S, Guthrie KI,
                                                                                                                                                                                                                                                                                                                                                                    (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-424396/45.
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PF 16-SEP-2003; 2003US-00663589.

XX
PR 27-SEP-2002; 2002US-0414441P.
XX
(HEIL/) HEILMAN D.
PA (DiJJ/) DI J.
XX
XX
Heilman D, Di J, Bray B;
XX
WPI; 2004-339372/31.
XX
Pharmaccutical composition used to treat Human Immunodeficiency Virus Comprises solution comprising synthetic peptide (Human Immunodeficiency Virus fusion inhibitor) in mixture with polyol.
XX
PT Prosprises solution comprising synthetic peptide (Human Immunodeficiency Virus fusion inhibitor) in mixture with polyol.
XX
CC The present invention relates to a pharmaccutical composition comprised CC of polymer admixed with synthetic peptides derived from human immunodeficiency virus (HIV) gp41. The invention is useful in treating CC C the invention
XX
CC C The invention
XX
CC C The invention
XX
CC C The invention
XX
Sequence 36 AA;
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0; Gaps

Ouery Match 100.0%; Score 192; DB 8; Length 36; Best Local Similarity 100.0%; Pred. No. 2.1e-16; Matches 36; Conservative 0; Mismatches 0; Indels

1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

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Search completed: March 6, 2006, 15:37:21 Job time : 115.667 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March Run on:

6, 2006, 15:37:45 ; Search time 18.3333 Seconds (without alignments) 188.935 Million cell updates/sec

US-09-809-060A-4

192 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

11837

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	myosin regulatory			R2R3-MYB transcrip	hemoglobin AII - t	renin-2 - mouse (f	hypothetical prote	hemoglobin BII - t	hypothetical prote	hypothetical prote		hypothetical prote	c	hypothetical prote	5.7K hypothetical	cystic fibrosis tr	hypothetical prote			_		н	hypothetical prote	gene 60 protein -	hypothetical prote		thymosin beta-12 -	hypothetical prote	probable NADPH-fer
SUMMARIES	ID	A345	H70152		-						D83682		C81237					77777S				G84063					S21282	S21694	D83774	T06541
	DB														0			7												0
	Length	36	ž	33	45	24	ž	38	4	æ	36	4	4	4	ŭ	ž	48	40	4	41	4	4.7	တိ	4	4	33	43	4	4	20
de	Query Match	٦.	20.3	19.8	•	ъ.	٠.	18.8	18.8	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.0	17.7	17.7	17.7	17.7	17.7	17.7	17.4	•	•	•	•	17.2	17.2
	Score		39	38		36	36	36	36	35	35	32	35	35	35	35	34.5	34	34	34	34	34	34	33.5	ω.		33	33	33	33
	Result No.	1	~	٣	4	ស	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

ribosomal protein	thymosin beta-4 -	hypothetical prote	hypothetical prote	thymosin beta-4 (v	thymosin beta-4 -	L33 protein (impor	hypothetical prote	thymosin beta-4 -	50S ribosomal prot	phospholipase A2 (trp operon leader	calreticulin, uter	hypothetical prote	Ig heavy chain V r
D90534	TNBOB4	T07503	H83653	A38682	TNRTB4	E97287	F70221	A37217	A90573	868897	LFSEW	E33208	H82533	S20771
70	٠.	~	N	н	н	Ŋ	~	-	~	~	н	~	~	~
9 4 6	43	43	43	44	44	49	49	20	20	25	28	53	31	32
16.9	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.1	16.1	16.1	16.1	16.1
32.5	32	32	32	32	32	32	32	32	32	31	31	31	31	31
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Fil/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental Fil/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental Fi2Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental F;9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status experimental F;18/Binding site: phosphate (Thr) (covalent) (by myosin-light-chain kinase) (partial) #F;19/Binding site: phosphate (Thr) (covalent) (by myosin-light-chain kinase) (partial) #F;19/Binding site: phosphate (Ser) (covalent) (by myosin-light-chain kinase) #status exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Experimental gource: platelet
R,Colburn, J.C.; Michnoff, C.H.; Hsu, L.C.; Slaughter, C.A.; Kamm, K.E.; Stull, J.T.
J. Biol. Chem. 263, 19166-19173, 1988
A,Title: Sites phosphorylated in myosin light chain in contracting smooth muscle.
A,Reference number: A31967; MUID:89066722; PMID:3198618
                                                                                            C.Date: 29-Jun-1990 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004 C.Accession: A34594; A31967  
R.IRebe, M.; Reardon, S. Bickhemistry 29, 2713-2720, 1990  
A.Title: Phosphorylation of bovine platelet myosin by protein kinase C. A.Reference number: A34594; MUID:90268021; PMID:2346743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-33,'X',35-36 <IKE>
A;Cross-references: UNIPROT:Q7M2V5; UNIPARC:UPI00001776D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: blocked amino end; EF hand; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Experimental source: smooth muscle
C, Superfamily: calmodulin; calmodulin repeat homology
nyosin regulatory light chain - bovine (fragment)
                                                            (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPARC: UPI00001776DA
                                                      C; Species: Bos primigenius taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 17-34 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A34594
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2 TSLIYSLLEKSQIQOEK 18 || :::: ::||||: | TSNVFAMFDQSQIQEFK 34 18

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20.8%; Score 40; DB 2; Length 36; 41.2%; Pred. No. 1.8e+02;

Query Match
Best Local Similarity 41.2
Matches 7; Conservative

RESULT

hypothetical protein BB0425 - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

R.Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997 C; Accession: H70152

Vugt, B.

White

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Gaps

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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: I77411
R;Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W
Mol. Cell. Biol. 4, 2321-2331, 1984
Mol. Cell. Biol. 4, 2321-2331, 1984
A;Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analys
A;Reference number: I57576; MUID:85085936; PMID:6392850
A;Accession: I77411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P00796; UNIPARC:UPI000016C94B; GB:K02801; NID:g200695; PIDN:A:
C;Superfamily: Pepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Risuzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
A;Reference number: S01807; MUID:89076216; PMID:3202832
A;Accession: S01808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hemoglobin AII - tube worm (Lamellibrachia sp.) (fragment)
C;Species: Lamellibrachia sp.
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: S01808
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C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C.Accession: C82373
  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-45 <RO2>
A;Cross-references: UNIPARC:UP1000016DC6F; EMBL:295788; PIDN:CAB09220.1
C;Genetics:
A;Gene: MYB56; MYB65
                                                                                                                                                                                            Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
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Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 1-24 <80Uz>
A;Cross-references: UNIPROT::Q9TWS6; UNIPARC:UPI000017711B
C;Keywords: oxygen carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2; Ler
Pred. No. 3.6e+02;
                                                                                                                                                                                    Score 37; DB 2; Le
Pred. No. 5.5e+02;
7; Mismatches 6;
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                                                                                                                                                                                                                                                                                               9 LEKSQIQQEKNEQELLEL----DKWASL 32
                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
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26.3%;
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Best Local Similarity 34.5%;
Matches 10; Conservative
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A; Residues: 1-30 < RES>
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A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID: 98065943; PMID: 9403685
A; Accession: H70152
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-30 KLEs
A; Esterences: UNIPROT: O51386; UNIPARC: UPI0000057491; GB: AE001147; GB: AE000783; NID
A; Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myosin light chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150390; 150392
R;Winter, B.; Klapthor, H.; Wiebauer, K.; Delius, H.; Arnold, H.H.
J. Biol. Chem. 260, 4478-4483, 1985
M;Title: Isolation and characterization of the chicken cardiac myosin light chain (L-2A)
A;Reference number: 150390; MUID:85157617; PMID:2984206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Zarraga, A.
J. Biol. Chem. 261, 13852-13860, 1986
J. Biol. Chem. 261, 13852-13860, 1986
J. Litle: Characterization of 5'-flanking region of myosin light chain 2A gene: Structura A;Reference number: 150392; MUID:87008629; PMID:3020054
A;Accession: 150392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-31 <2AR>
A;Cross-references: UNIPARC:UPI00000FD6CF; GB:J02587; NID:g212390; PIDN:AAA48977.1; PID:C;Genetics: 1/3
C;Genetics: 1/3
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q91828; UNIPARC:UPI00000FD6CF; GB:M10990; NID:g212385; PIDN:
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                                                                                                                                                                                                                                                                    Length 30;
                                                                                                                                                                                                                                                                                                                    3; Indels
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A;Molecule type: DNA
A;Residues: 1-31 <WIN>
                                                                                                                                                                                                                                                                  Score 39; DB 2;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                  20.3%;
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15 SNVFSMFEQAQIQEFK 30
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8 ELSKVKSOKNKONLL 22
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Best Local Similarity 46.7
Matches 7; Conservative
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Best Local Similarity 43.8
Matches 7; Conservative
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA,
A;Residues: 1-36 &STO>
A;Crose-references: UNIPROT:Q9KG53; UNIPARC:UPI0000139521; GB:AP001507; GB:BA000004; NID
A;Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C'Accession: C81237
Tyettellin, H.; Saunders, N.J.; Heidelberg, J.; Jaffries, A.C.; Nelson, K.E.; Eisen, J.A Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: UNIPARC:UP1000011E471; EMBL:AB001684; NID:92224352; PIDN:BAAS7939.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the green alga
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C;Species: chloroplast Chlorella vulgaris
C;Aacession: 19799 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Aacession: T07291
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuk
Proc. Natl. Acad. Sci. U.S.A. 94, S967-5972, 1997
A;Title: Complete nucleoride sequence of the chloroplast genome from the gree
A;Reference number: 215985; MUID:97303241; PMID:9159184
                                                                                                                                                                                                                                                                                                                                            C,Species: Bacillus halodurans
C,Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                   aypothetical protein BH0260 [imported] - Bacillus halodurans (strain C-125)
                                              Gaps
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                                              Indels
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               Best Local Similarity 31.8%; Pred. No. 6.8e
Matches 7; Conservative 6; Mismatches
                                                                                                         1 YTSLIYSLLEKSQIQQEKNEQE 22
                                                                                                                                           12 YINMSAGLMKWANTQQLSTERE 33
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Best Local Similarity
Matches 7; Conserv
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A62035; MUID:20406833; PMID:10952301
A;Status: president cype: DNA
A;Residues: 1-38 cHEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemoglobin BII - tube worm (Lamellibrachia sp.) (fragment)
C;Species: Lamellibrachia sp.
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-May-2004
C;Accession: S01814
R;Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
A;Reference number: S01807; MUID:89076216; PMID:3202832
                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9KVX1; UNIPARC:UP100000C2B91; GB:AE004094; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82186
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID: 20406833; PMID: 10952301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
6e+02;
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Pred. No. 6e+02
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-45 <SUZ>
A;Cross-references: UNIPARC:UP1000017711A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 EDRREMQLM----WANVWS 22
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Matches 5, Conservative
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Best Local Similarity 46.7
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-33 <HEI>
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A; Status: preliminary
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                                       Similarity
8; Conserv
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Job time: 19.3333 secs
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A;Residues: 1-50 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             high light-inducible protein homolog - Cyanophora paradoxa cyanelle
C;Species: cyanelle Cyanophora paradoxa
C;Species: cyanelle Cyanophora paradoxa
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06929
R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
Submitted to the EMBL Data Library, July 1995
A;Scaription: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A;Reference number: 215840
A;Accession: T06923
A;Reference number: 215840
A;Accession: T06923
A;Reference: DNA
A;Residues: 1-49 <STI.
A;Residues: 1-49 <STI.
A;Cross-references: UNIPROT:P48367; UNIPARC:UP1000013A441; EMBL:U30821; NID:g1016083; PI
A;Experimental source: strain Pringsheim LB555
C;Genetics:
A;Gene: ycf17
Science 287, 1809-1815, 2000

A,Authors: Grandi, G.; Sun, D.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ve A,Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.

A,Reference number: A81000; MUID:20175755; PMID:10710307

A,Status: preliminary

A,Status: preliminary

A,Residues: 1-47 < TET>

A,Residues: 1-47 < TET>

A,Residues: 1-47 < TET>

C,Coserience: UNIPROT:09K114; UNIPARC:UPI00000C43EE; GB:AE002369; GB:AE002098; NID

C,Genetics:
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B90557
hypothetical protein MYPU_3650 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C; Species: Mycoplasma pulmonis
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C; Accession: B90557
R; Chambaud, 1.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A; Reference number: A99512; MUID:21267165; PMID:11353084
A; Residues: preliminary
A; Molecula type: DNA
A; Residues: 1-50 < KUR>
A; Residues: 1-50 < KUR>
A; Cross-references: UNIPROT:098QJ6; UNIPARC:UPI0000C8071; GB:AL445566; PID:gl4089779; E
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                               Length 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 2;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 EKSOJOO----EKNEGELLELDKW 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 ККООТООККЕТЕКЅРКНКАЅКООМ 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 IQQEKNEQELLELDKWASLWNW 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IWNW 10
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
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Matches 6; Conserv
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A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                  A;Gene: NMB0099
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Chaccesion: F86472
RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: Q9C6E9; UNIPARC: UPI00000A80F1; GB: AE005172; NID: 911386311; P
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                                                                                                                                                                                                                                                                                                                                                                                    5.7K hypothetical protein T32G9.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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Length 50;
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Score 35; DB 2; Pred. No. 1.1e+03;
                                                                      5; Mismatches
                                                                                                                                                                                    6 LYENIKKEKIYKSKNSIVLNEFKK 29
                                                                                                                                            5 IYSLLEKSQIQQEKNEQELLELDK 28
18.2%;
33.3%;
                                                                         Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model Run on:

6, 2006, 15:31:50 ; Search time 116.667 Seconds (without alignments) 217.706 Million cell updates/sec March

US-09-809-060A-4 Perfect score:

1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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tion	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	tetra	plasm	bacillus	spele	crice	nasut	vibri	plati	bacte	พนธ น	bacil
Description	069895	968690	606690	069910	906690	069907	069893	069908	069894	069905	069903	069898	Q69904	069899	006690	069891	069901	069902	069892	069897	Q4t4h4	04yjt6	Q732e0	Q68ky9	059118	O9xxw6	Q87jd4	Q98tj0	Q4zbq6	Q675b2	062sn1
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	9HIV1	_9HIV	_9HIV	_9HIV	_9HIV	_9HIV]	_9HIV	8_9HIV1	_9HIV	_9HIV	9HIV	9HIV	_9HIV	_9HIV	_9HIV	_9HIV	_9HIV	_9HIV	_9HIV	PHIV	TEIN	PLAB	BACC	9CRU	CRIG	9NEOP	VIBPA	PLAF	9VIR	MOUS	BACLD
£	069895	Q69896_9HIV1	606690	Q69910_9HIV1	906690	069907	Q69893_9HIV1	069908	069894	Q69905_9HIV1	Q69903 9HIV	Q69898 9HIV	069904	069899	Q69900_9HIV1	Q69891_9HIV	Q69901_9HIV3	Q69902_9HIV1	Q69892_9HIV1	Q69897_9HIV1	Q4T4H4	Q4YJT6_PLABE	Q732E0_BACC1	Q6SKY9	QSQ1L8 CRIGR	9MXX60	Q87JD4	Q98TJO_PLAFE	Q4ZBQ6_9VIRU	Q675B2	062SN1
DB	7	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	7	~	~				N	~	~	~	~
% Query Match Length	49	49	49	42	49	49	34	49	34	34	34	20	34	20	20	41	47	48	41	29	48	41	42	20	47	43	43	48	49	30	47
* Query Match	94.3	94.3	92.7	91.7	90.6	89.1	88.0	88.0	87.5	86.5	85.4	84.9	82.3	81.8	81.8	77.6	76.0	76.0	75.5	68.8		24.0	24.0	23.7	23.4	22.4	22.4	22.4	22.4	22.1	22.1
Score	181	181	178	176	174	171	169	169	168	9	9	163	158	157	157	149	146	146	145		20	46	46	45.5	45	43	43	43	43	42.5	42.5
Result No.	1	7	e	4	'n	9	7	80	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31

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	AA.	ALIGNMENTS RET; 49	ALIGI PRT;			V1	HIV1 895_9	RESULT 1 069895_9HIV1 1D 069895_
Q68wb8 rickettsia		RICTY	Q68WB8_RICTY	α.	0.3 46	~	39	45
Q4hnwl campylobact		CAMUP	Q4HNW1	~	0.3 44	N	39	44
Q6sz29 streptococc		STRPY	Q6SZ29 STRPY	N	20.3 44	~	39	43
Q9eq12 mus musculu		400SE	Q9EQ12 MOUSE	N	20.3 31	N	39	42
_		RBU	Y425 BORBU	-	•	N	39	41
Q672j0 pennisetum		PENAM	Q672J0_PENAM	N	20.3 27	N	39	40
OSh795 hodotermops		NEOP	Q5H795 9NEOP	~	•	N	40	39
Q56z83 arabidopsis		ARATH	Q56Z83 ARATH	7		N	40	38
Q7m2v5 bos taurus		SOVIN	Q7M2VS_BOVIN	~	20.8 36	N	40	37
Q8cgr6 staphylococ		STAEP	Q8CQR6_STAE	~	21.4 38	N	41	36
Q5hrw7 staphylococ		STAEQ	QSHRW7 STAE	7	21.4 38	~	41	35
Q905j7 human immun		HIVI	V1H6_75060	N	21.4 36	N	41	34
P82214 bombyx mori		SOMMO	P82214 BOMM	N	21.4 30	~	41	33
Q8m2c8 pyrocoelia		PYRRU	Q8M2C8_PYRR	ď	1.6 50	N	41.5	32

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Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.M. Booce L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 AA; 6168 MW; 8077C4815B83281E CRC64;
                                                                                                                                                                                                                                                                                                                                  GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 YTGLIYTLLEESQIQQEKOREQELLELDKWASLWNWF 49
                                                                                                                                                                                                                                                                       monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994)
EMBL; U06725; AAA19138.1; -; mRNA.
HSSP; P31872; 1LBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 181; DB 2;
Pred. No. 1.1e-14;
2; Mismatches 1;
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91.7%;
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NON TER 1 1
NON TER 49 49
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Best Local Similarity
Matches 33; Conserv
                                                              Gp41 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Last sequence update) Last annotation update) 49 AA. Created) PRT; Q69896_9HIV1 PRELIMINARY; C Q69896_ 01-NOV-1996 (TEMBLrel. 01, 01-NOV-1996 (TEMBLrel. 01, 01-JUN-2003 (TEMBLrel. 24, Gp41 (Fragment)
Name=env;

Human immunodeficiency virus 1. Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.

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SEQUENCE
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NON TER
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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MICLEOTIDE SEQUENCE.

CONIEY A.J., FRESIGN.

CONIEY A.J., SRAW A.R., BOOCTS L.J., Tung J.S., Arnold B.A.,

Keller P.M., Shaw A.R., Emini E.A.;

Wouriants and primary isolates by IAM-41-2F5, an anti-gp41 human monoclonal antibody.";

Emonoclonal antibody.";

EMBL, U06739; AAA19152.1; -; mRNA.
                                                                    MEDLINE=94211861; PubMed=7512731;

Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL: U06726; AAA19139.1; -; mRNA.
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Pred. No. 1.1e-14;
2; Mismatches 1; Indels
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GG; GG:0019031; C:viral envelope; IEA.
GG; GG:0019031; C:viral envelope; IEA.
InterPro; IPRO0328; Env_GP41.
Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                            GO; GO:0016021; C:integral to membrane; IEA.
60; GO:0019031; C:viral envelope; IEA.
60; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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Last annotation update)
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Pred. No. 2.5e-14;
1; Mismatches 2;
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Best Local Similarity 91.7%;
Matches 33; Conservative
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09_9HIV1
Q69909_9HIV1_PRELIMINARY;
Q69909;
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Matches 33, Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00517; GP41; 1
                                                  SEQUENCE
NCBI_TaxID=11676;
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RESULT 4

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Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
MCLOTLEY A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A., Keller P.M., Shaw A.K., Emini E. M., Emini E. J., Tung J.S., Arnold B.A., "Neutralization of divergent human immunodeficiency virus type 1 variants and primary isolates by IAM-41-2F5, an anti-gp41 human monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL; U06740; AAAA19153.1; -; mRNA.
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Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 42;
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EMBL, U06736; AAA19149.1; -; mRNA.

HSSP; P31872; ILBO.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IRR00328; Env GP41.

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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
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Last annotation update)
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Pred. No. 3.7e-14;
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Q69910 9HIV1 PRELIMINARY;
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nes 31; Conserv
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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EMBL; U06737; AAAA9150.1; -; mRNA.
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Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.,
"Neutralization of divergent human immunodeficiency virus type
                              Score 174; DB 2; Length 49;
Pred. No. 7.8e-14;
4; Mismatches 1; Indels
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPRO0328; Env_GP41.
Pfam; PF00517; GP41; 1.
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Pred. No. 1.8e-13;
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                                  90.6%;
86.1%;
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nilarity 83.3%;
Conservative 5
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Q69893;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q69907_9HIV1 PRELIMINARY;
Q69907;
                                                                                                            31; Conservative
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wes 30; Conserv
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                                  Query Match
Best Local
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069907 9H
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DO 60698 AC 60698
DD 01-N

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Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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MEDILIPE-94211861, PubMed-7512731,

CONLEY A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,

Keller P.M., Shaw A.R., Emini E.A.;

"Neutralization of divergent human immunodeficiency virus type 1

variants and primary isolates by IAM-41-2F5, an anti-gp41 human

monoclonal antibody.";
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Pred. No. 3.2e-13;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                              88.0%; Score 169; DB 2; Length 34; 93.9%; Pred. No. 2.2e-13;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
                                                                          GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:vixal envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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Last sequence update)
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Last annotation update)
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         Acad. Sci. U.S.A. 91:3348-3352(1994)
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EMBL; U06738; AAA19151.1; -; mRNA.
HSSP; Q87973; 2SIV.
                                                                                                                                                                                                                                                                                                                                                                                               4 LIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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Query Match

Best Local Similarity 83.3%;
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q69908 9HIV1 PRELIMINARY;
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Q69894;
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NUCLEOTIDE SEQUENCE
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Matches 30; Conserv
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
  Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
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MEDLINE-942.1861; PubMed=7512731;

Conley A.J., Keseller J.A., Boots L.J., Tung J.S., Arnold B.A.,

Conley A.J., Keseller J.A., Boots L.J., Tung J.S., Arnold B.A.,

A Keller P.M., Shaw A.R., Emini E.A.;

"Neutralization of divergent human immunodeficiency virus type 1

variants and primary isolates by IAM-41-2F5, an anti-gp41 human

T monoclonal antibody.";

Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).

R EMBL 106735; AAA19148.1; -; mRNA.

R HSSP; P31872; ILBG

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001599; F:structural molecule activity; IEA.

R GO; GO:000328; Extructural molecule activity; IEA.

R Pfam; PF00517; GP41; 1.
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                                                                                                NUCLEOTIDE SEQUENCE.
MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
Medler P.M., Shaw A.R., Emini E.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.J., Tung J.S., Arnold B.A.,
Medler P.M., Shaw A.R., Emini E.J., and J.S., Arnold B.A.,
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL, U06724; AAA19137.1; -; mRNA.
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Pred. No. 5e-13;
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                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                          Lentivirus; Primate lentivirus group
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1 Similarity 93.9%;
31; Conservative 1
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Q69905;
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Matches 30; Conserv
                                             NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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MEDILINE-94211861; PubMed-7512731;

MEDILINE-94211861; PubMed-7512731;

A Keller P.M., Shaw A.R., Boots L.J., Tung J.S., Arnold B.A.,

Keller P.M., Shaw A.R., Emini E.A.;

"Neutralization of divergent human immunodeficiency virus type 1

variants and primary isolates by IAM-41-2F5, an anti-gp41 human

"Throc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).

EMBL, U06728; AAA11941.1; -; mRNA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

REPRINTED CO:0019031; C:viral envelope; IEA.
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Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.J.,
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL; U06733; AAA19146.1; -; mRNA.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0001919; F:structural molecule activity; IEA.
Interv.; IPRO00328; Env_GP41.
Pfam; PF00517; GP41; 1.
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88.2%; Pred. No. 8.9e-13;
Live 3; Mismatches 1;
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              34 AA
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Q69903_9HIV1 PRELIMINARY;
Q69903;
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Q69898;
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monoclonal antibody.
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Job time: 117.667 secs
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
                                                       Gaps
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MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
Keller P.M., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL; U06734; AAAA1147.1; -; mRNA.
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MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Colley A.J., Kessler J.A., Enini E.A.;
Keller P.M., Slaw A.R., Enini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1 variants and primary isolates by IAM-41-2F5, an anti-gp41 human
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EABA093A1C6C79E1 CRC64;
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GO; GO:0019031; C:viral errelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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Last annotation update)
                          Score 163; DB 2; Le
Pred. No. 1.8e-12;
4; Mismatches 3;
                                                                                                15 YTGYIYNLLEESQNQQEKCNEQDLLELDKWANLWNWF 50
                                                                                 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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Pred. No. 4.8e-12;
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84.8%;
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01-JUN-2003 (TrEMBLrel. 24,
6358 MW;
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Q69899 9HIV1 PRELIMINARY;
Q69899;
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Q69904_;
                     Query Match
Best Local Similarity 80.6
Matches 29; Conservative
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Name=env;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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                                             GG); GO: 0016021; C: integral to membrane; IEA.
GG); GO: 0019031; C: viral envelope; IEA.
GO; GO: 0019031; C: viral envelope; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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SEQUENCE 50 AA; 6287 MW; EABA093F0877D85B CRC64;
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EMBL; U06730; AAA19143.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; E:viral molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994)
EMBL; U06729; AAA19142.1; -; mRNA.
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77.8%; Pred. No. 9.8e-12;
tive 4; Mismatches 4,
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ID Q69900 9HIV1 PRELIMINARY;
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Matches 28; Conservative
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6, 2006, 15:43:16

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Sequence 1360, Ap Sequence 1360, Ap Sequence 1360, Ap Sequence 1360, Ap Sequence 1360, Ap Sequence 1361, Ap Sequence 5, Appli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 240, App
Sequence 1360, Ap
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    (without alignments)
    107.578 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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1 YTSLIYSLLEKSQIQQEKONEQELLELDKWASLWNWF
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US-09-082-279B-1360
US-09-135-304B-1360
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US-09-135-641C-1360
US-09-135-641C-1360
US-09-135-965A-1361
US-09-135-304B-1361
US-09-135-304B-1361
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 5, Appl Sequence 153, A Sequence 5, Appl Sequence 1423, P Sequence 1423, P Sequence 1423, P Sequence 1749, P Sequence 1938, P Sequence 642, A Sequence 642, A		INCLUDING HIV
4 36 2 US-08-485-546A-5 4 36 2 US-09-515-965A-1553 4 36 2 US-09-515-961A-1554 4 36 2 US-09-623-186A-5 4 36 2 US-10-625-136-5 4 36 2 US-10-625-136-5 4 36 2 US-09-637-276-1423 3 2 US-09-515-965A-1986 3 36 2 US-09-350-641C-1749 3 36 2 US-09-350-641C-1749 3 36 2 US-09-315-364B-642 3 6 2 US-09-315-304B-642 3 6 2 US-09-315-304B-642	ALIGNMENTS	RESULT 1 US-08-444-223B-240 US-08-444-223B-240 Sequence 240, Application US/0848423B Patent No. 6020459 GENERAL INCORMATION: APPLICANT: Bolognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Matthews, Thomas J. APPLICANT: Lambert, Dennis M. APPLICANT: Lambert, Dennis W. APPLICANT: Lambert, Dennis W. APPLICANT: Lambert, Dennis G. TITLE OF INVENTION: COMPOSITIONS: COMPOSITIONS: COMPOSITIONS: APPLICANT: Langlois, A. Albhonses J. Albhonses J. Albhonses J. APPLICANT: Langlois, A. Albhonses J. Albhonses
187 97 1887 97 1887 97 1887 97 1887 97 1887 97 1881 94 181 94 179 93 179 93 179 93 179 93		SGUT 1 Sequence 240, Application Batent No. 6020459 GENERAL INCREMATION: APPLICANT: Balognesi, APPLICANT: Matchews, APPLICANT: Matchews, APPLICANT: Matchews, APPLICANT: Barney, Sh APPLICANT: Lambert, DAPLICANT: Lambert, DAPLICANTON: TITLE OF INVENTION: USA ZIP: 10036-2711 COMPUTES: New YORK STRATE: New YORK COUNTRY: USA ZIP: 10036-2711 COMPUTES: LENGY MEDIUM TYPE: Flopy COMPUTES: BAPLICATION DA APPLICATION NUMBER: REFERENCE CALLATION: 435 ATTORNEY/ABRAITION NUMBER: RESIEFRENCE/DOCKET NUM TELEPAN: (212) 79 TELEPHONE: METALERICANTON TELEPHONE: (212) 79
8 0 0 1 1 1 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4		RESULT 1 US-08-484-223B- Sequence 240, Petent No. 60 GENERAL INFO GENERAL INFO APPLICANT: CONPUTER OF INTIME OF IN

Length 36;

DB 2;

100.0%; Score 192;

Query Match

TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-484-223B-240

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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 36; Conservative
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APPLICANT: Barney, S.
APPLICANT: Barney, G.
APPLICANT: Marct, M.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 1972-05.2
CURRENT APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667-20
SOFTWARE FRAISEQ for Windows Version 3.0
SEQ ID NO 1360
LENGTH: 36
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100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels
                         Indels
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APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT FILING DATE: 1996-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1360
LENGTH: 36
  L Similarity 100.0%; Pred. No. 1e-16; 36; Conservative 0; Mismatches 0;
                                                                                                 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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                                                                   1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                  Sequence 1360, Application US/09082279B Patent No. 6258782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1360, Application US/09315304B Patent No. 6348568
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ORGANISM: Artificial Sequence
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APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
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US-09-082-279B-1360
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US-09-315-304B-1360
Best Local
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APPLICANT: Antcrark, J.
APPLICANT: Antcrark, J.
APPLICANT: Delmedico, M.
APPLICANT: Exickson, J.
APPLICANT: Exickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERRINCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR PLING DATE: 1999-05-20
PRIOR PELICATION NUMBER: 09/082,279
PRIOR PELICATION NUMBER: 09/082,279
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1360
LENGTH: 36
LENGTH: 36
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APPLICANT: Guthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amerr, Mohmed
APPLICANT: Lambert, Dennis
ITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
ITLE OF INVENTION: HYBRID POLYPEPTIDES
ITLE OF INVENTION: 1912-043
CURRENT APPLICATION NUMBER: 109/081,784
CURRENT FILING DATE: 1998-05-20
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1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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; Sequence 1360, Application US/09515965A
; Patent No. 6623741
                                                                                                                                                                                                                                                                      Sequence 1360, Application US/09834784
Patent No. 6562787
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APPLICANT: Anwer, Mohmed
APPLICANT: Lamber, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YTSLIYSLLEKSQIQQEKNEQELLQLDKWASLWNWF 36
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                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/082,279B CURRENT FILING DATE: 1998-05-20 NUMBER OF SEQ ID NOS: 1515 SSCTWARE: RattSEQ for Windows Version 3.0 LENGTH: 36
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1361
LENGTH: 36
                   Patent No. 6258782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1361, Application US/09315304B
Patent No. 6348568
                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Core polypeptide US-09-082-279B-1361
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                           7872-043
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APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 35; Conserv
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                 -09-082-279B-1361
                                                                                                                                                                                                                               FILE REFERENCE:
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US-09-834-784-1361
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TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 36;
                   1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 192; DB 2 100.0%; Pred. No. 1e-16;
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/350,641C CURRENT FILING DATE: 1999-07-09 PRIOR APPLICATION NUMBER: 09/315,304 PRIOR FILING DATE: 1999-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1360
                                                                                                         US-09-350-641C-1360
; Sequence 1360, Application US/09350641C
; Patent No. 6656906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Core polypeptide US-09-350-841A-1360
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Core polypeptide US-09-350-641C-1360
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                           Guthrie, K.
Merutka, G.
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Best Local Similarity
Matches 36; Conserv
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Best Local Similarity
Matches 36; Conserv
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APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT PILLING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
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Pred. No. 2.4e-16;
1; Mismatches 0
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US-09-350-841A-1361
            -09-350-641C-1361
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Sequence 1361, Application US/09515965A

Patent No. 6623741

GENERAL INFORMATION:

APPLICANT: Antczak, J.

APPLICANT: Exickson, J.

APPLICANT: Lambert, D.

APPLICANT: Lambert, D.

APPLICANT: Lambert, D.

APPLICANT: Lambert, D.

TITLE OF INVENTION: MSSOCIATED EVENTS INCLUDING RSV TRANSMISSION

TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION

FILE REFERENCE: 7872-073

CURRENT FILING DATE: 1200-02-29

PRIOR PLILNG DATE: 1999-05-20

PRIOR PLILNG DATE: 1999-05-20

PRIOR FILING DATE: 1998-05-20

PRIOR FILING DATE: 1998-05-20

PRIOR FILING DATE: 1998-05-20

WUMBER OF SEQ ID NOS: 1994

SOUTHWARE: FESTEGE FOR WINDOWS Version 3.0
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APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: HYBRID: 18/09/834,784

CURRENT APPLICATION NUMBER: US/09/834,784

CURRENT PILING DATE: 19001-04-13

FRIOR APPLICATION NUMBER: 09/082,279

FRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SEQ ID NO 1361

LENGTH: 36
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ilarity 97.2%; Pred. No. 2.4e-16;
Conservative 1; Mismatches 0
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Sequence 1361, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Core polypeptide US-09-834-784-1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Core polypeptide US-09-515-965A-1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 35; Conserva<sup>†</sup>
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LENGTH: 36
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RESULT 12

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Patent No. 6750008

GENERAL INFORMATION:
APPLICANTION:
APPLICANTION:
APPLICANTION:
APPLICANTION:
APPLICANTION:
TITLE OF INVENTION:
FILE REPERENCE: 7872-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT APPLICATION NUMBER: US/09/350,841A
SEQ ID NOS: 1946
SEQ ID NO 1361
LENGTH: 36
                                                                         APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Ambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRER: US/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/0115,304
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PELING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FRAESEQ FOR Windows Version 3.0
SOFTWARE: FRAESEQ FOR Windows Version 3.0
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Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 1; Mismatches 0;
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Sequence 1361, Application US/09350641C Patent No. 6656906 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Core polypeptide US-09-350-841A-1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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6, 2006, 15:45:44
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US-08-486-099-5
                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
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Job time : 27.6667 secs
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Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF
VENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                               TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV TITLE OF INVENTION: TRANSMISSION NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,028
FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                    STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: USA ZIP: 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155 Avenue of the Americas
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08486099
Patent No. 6013263
Matthews, Thomas J.
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Matthews, Thomas J.
Wild, Carl T.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.2
Matches 35; Conservative
                  Wild, Carl T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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STATE: New York
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APPLICANT: Bologn
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STREET: 11
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YTSLIYSLLEKSQTQQEKNEQELLELDKWASLWNWF 36
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Pred. No. 4.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                        SOFTWARE: Patentin Release T. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099 FILING DATE: 07-JUN-1995
CIASSIFTCATION: 435
ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, LAUTA A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELERAX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGRH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.2%;
Matches 35; Conservative
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1, Appli 108, App 16, Appli 1, Appli 1, Appli 37, Appli 39, Appli 8, Appli 10, Appli

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Sequence 1 Sequence 1 Sequence 3 Sequence 3 Sequence 3 Sequence 8

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Perfect score:

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Score

Result No.

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Publication No. US20050065319A1
GENERAL INFORMATION:
APPLICANT: Baroudy, Bahige M.
TITLE OF INVENTION: Combination Method For Treating Viral Infections
FILE REPRENENCE: 1801358
CURRENT APPLICATION NUMBER: US/10/168,295
CURRENT FILING DATE: 2002-06-19
PRIOR PILING DATE: 2000-12-17
PRIOR PELICATION NUMBER: 60/256,657
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTI VERSION 3.1
SOFTWARE: PATENTI VERSION 3.1
                                                                                                                                                                                                                                                                                                      | MS-10-168-295-5
| Sequence 5, Application US/10168295
| Sequence 5, Application NO. US2005065319A1
| Publication No. US20050065319A1
| GENERAL INFORMATION:
| APPLICANT: Baroudy, Bahige M.
| TITLE OF INVENTION: Combination Method For Treating Viral Infections
| FILE REFERENCE: IN01358
| CURRENT APPLICATION NUMBER: US/10/168,295
| CURRENT APPLICATION NUMBER: US/206-19
| PRIOR PILING DATE: 2002-06-19
| PRIOR PILING DATE: 2000-12-17
| PRIOR FILING DATE: 2000-12-19
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin Version 3.1
| SEQ ID NO 5
| LENGTH: 36
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                                                                                         DB 4; Length 36;
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                                                                                                                                                                                                        1 YTSLIYSLLEKSQIQQEKVEQELELDKWASLWNWF 36
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100.0%; Score 192; DB 5;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                       Score 192; DB 4
Pred. No. 3e-15;
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US-10-168-295-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                   0; Mismatches
                    ; OTHER INFORMATION: synthesized US-10-671-282-40
                                                                                       100.0%;
ilarity 100.0%;
Conservative 0
                                                                                       Query Match
Best Local Similarity
Matches 36; Conserv
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FEATURE:
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TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and TITLE OF INVENTION: Their use in therapy
FILE REFERENCE: TRA-004

CURRENT APPLICATION NUMBER: US/10/671,282

CURRENT APPLICATION NUMBER: 00/414,439

PRIOR RILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 114

SEQ ID NO 40

LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
TITLE OF INVENTION: Gp41-derived peptides, and its use in therapy
TITLE OF INVENTION: Gp41-derived peptides, and its use in therapy
FILE REFERENCE: TRA-003
FILE REFERENCE: TRA-003
CURRENT FILING DATE: 2003-09-16
FRIOR APPLICATION NUMBER: US 60/414,441
FRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2
SEQ ID NO 40
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100.0%; Pred. No. 3e-15;
tive 0; Mismatches C
                PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 36
                                                                                                                                                                                                                   ) OTHER INFORMATION: Core polypeptide US-10-351-641-1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 40, Application US/10671282; Publication No. US20040122214A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: synthesized US-10-663-589-40
                                                                                                                                                                        ORGANISM: Artificial Sequence
FILING DATE: 1999-05-20
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0°
Matches 36; Conservative
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Best Local Similarity
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ORGANISM: Artificial
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ORGANISM: Artificial
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JS-10-267-682-5
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                                                                                                                             APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Anwert, M.
APPLICANT: Anwert, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
FILE REPRENCE: 7872-100
CURRENT FILING DATE: 1090-10-24
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
PRIOR PILING DATE: 1998-05-20
PRIOR PILING DATE: 1998-05-20
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Johnson, M. Ross
APPLICANT: Lombert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
TITLE OF INVENTION: VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 787-2036
CURRENT APPLICATION NUMBER: US/10/252,136
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/08/973,952
PRIOR FILING DATE: 1998-05-29
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Pred. No. 6.8e-15;
1; Mismatches 0
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; ORGANISM: Human immunodeficiency virus
US-10-252-136-5
                                           ; Sequence 1361, Application US/10351641; Publication No. US20030186874A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Core polypeptide US-10-351-641-1361
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ORGANISM: Artificial Sequence
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Best Local Similarity 97.2%;
Matches 35; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 36
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Best Local Similarity
Matches 35; Conserv
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FUSION-ASSOCIATED EVENTS, INCLUDING HIV
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PORTS:
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION NUMBER: US/08/484,223A
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAMM: COPULZI, LAUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 36;
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97.4%; Score 187; DB 4;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 869-9741/8864
                                                                                                                                                                           Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS
MEMBRANE FUSI
                                                                                                                                                                                                                                                                                                  TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognest, Dani P.
Mild, Carl T.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 790-9090
Sequence 5, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 36 amino acids
                                                                                                                                                    Barney, Shawn O.
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                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 239
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
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CTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide
US-10-950-010-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.4%; Score 187; DB 5; Length 36; Best Local Similarity 97.2%; Pred. No. 1.2e-14; Matches 35; Conservative 0; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 1999-09-10, NUMBER OF SEQ ID NOS: 545, SEQ ID NO 5, SEQ ID NO 5, LENGTH: 36
                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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US-10-351-641-1749
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                                                                                                                                                                                                                                                        TYPE: PRT
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                                    Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5. Application US/10950010; Publication No. US20050070475A1; GENERAL INFORMATION:

APPLICANT: BRIDON, Dominique P.; APPLICANT: BRIDON, Dominique P.; APPLICANT: BRIDON, Dominique P.; APPLICANT: BUDDSELLAB, Nissab.; APPLICANT: ROBITAILLE, Martin.; APPLICANT: NINECTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL.; TITLE OF INVENTION: INPECTION: FILE OF INVENTION: UNRER: US/10/950,010; FILE REFERENCE: 5008620015017(RDC-1512); CURRENT APPLICATION NUMBER: US/10/950,010; PRIOR FILING DATE: 2000-09-05; PRIOR FILING DATE: 2000-09-17; PRIOR FILING DATE: 2000-09-17; PRIOR FILING DATE: 1999-05-17; PRIOR FILING DATE: 1999-05-17
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CUNTRY: New York

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/267,748

FILING DATE: 08-Oct-2002

CLASSIFICATION NUMBER: US/08/484,223A

PRIOR APPLICATION NUMBER: US/08/484,223A

APPLICATION NUMBER: US/08/484,223A

ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFOR
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97.4%; Score 187; DB 4;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: «Unknown»
TOPOLOGY: unknown
MOLECTLE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-267-748-5
                                                                                                                                                                TRANSMISSION
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LENGTH: 36 amino acids
TYPE: amino acid
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 239
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US-10-950-010-5
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APPLICANT: Ezrin, Alan M.
APPLICANT: Ezrin, Alan M.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Holmes, Darren L.
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD TITLE OF INVENTION: 2006-202-25
FILE REFERENCE: 500862002301
CURRENT FILING DATE: 2006-02-25
PRIOR FILING DATE: 2006-03-25
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-10-15
PRIOR PRIOR APPLICATION NUMBER: 60/153,406
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR SEQ. ID NOS: 1617
SOFTWARE: PARCHIN VET. 2.1
SOFTWARE: PARCHIN VET. 2.1
   Gaps
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US-11-066-697-1423
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                                                               1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                             1 YISLIYSLLEKSQTQQEKNEQELLELDKWASLWNWF 36
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Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Meruka, G.
                                                                                                                                                                                                                                                                                             Sequence 1423, Application US/11066697, Publication No. US20050187159A1 GENERAL INFORMATION:
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## APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-100.

CURRENT FILING DATE: 2003-01-24

CURRENT FILING DATE: 1999-07-09

PRIOR PLICATION NUMBER: 09/350,641

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 1757

SOFTWARE: PASESEQ for Windows Version 3.0

SEQ ID NO 149

LENGTH: 36
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APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
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Pred. No. 5.8e-14;
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93.2%; Score 179; DB 4;
Best Local Similarity 91.7%; Pred. No. 9.9e-14;
Matches 33; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 642
LENGTH: 36
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PRIOR FILING DATE: 1999-05-20
PRIOR PPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Core polypeptide US-10-351-641-1749
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US-10-351-641-642
; Sequence 642, Application US/10351641
; Publication No. US20030186874A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 33; Conservative
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APPLICANT:
APPLICANT:
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RESULT 15 US-10-457-780-52

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APPLICANT: SERRES, Pierre-Francois
APPLICANT: MCSCA, Joseph
TITLE OF INVENTION: GP41 PEPTIDES AND METHODS BASED THEREON FOR INHIBITING HIV FUSION
TITLE OF INVENTION: TO TARGET CELLS
FILE REFERENCE: 118761
CURRENT APPLICATION NUMBER: US/10/457,780
FRICK APPLICATION NUMBER: US/46,268
PRIOR APPLICATION NUMBER: US 60/446,268
PRIOR APPLICATION NUMBER: US 60/413,919
PRIOR PILING DATE: 2003-02-10
PRIOR PELING DATE: 2002-09-27
PRIOR PELING DATE: 2002-09-27
PRIOR PELING DATE: 2002-09-07
SPRIOR PELING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE PRECENTIN VERSION 3.2
SEQ ID NO SE
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Pred. No. 9.9e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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91.7%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.77
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COTHER INFORMATION: Y36F
US-10-457-780-52
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Sequence 1, Application US/11029003
Publication No. US20050260194A1
GENERAL INFORMATION:
APPLICANT: PETERS, ROBERT T.
APPLICANT: RIVERAL, DAM R.
APPLICANT: RIVERAL, DAMEL S.
APPLICANT: STATTEL, ALAN J.
APPLICANT: STATTEL, ALAN J.
APPLICANT: STATTEL, ALAN J.
APPLICANT: GINVENTION: INMUNOSIOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
FILE REFERENCE: 08945.0007-01000
CURRENT APPLICATION NUMBER: US/11/029,003
CURRENT FILING DATE: 2005-01-05
                        US-11-029-003-1
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                                                                                                                                                (without alignments) 72.002 Million cell updates/sec
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Sequence 33,
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Sequence 3
Sequence 7
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Sequence 4
Sequence 4
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
                                                                                                                            March 6, 2006, 15:50:56; Search time 10 Seconds
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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US-11-151-598-4

US-11-112-277-6

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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Maximum DB seq length: 50
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Sequence 13381, A Sequence 12322, A Sequence 12922, A Sequence 103, App Sequence 7039, App Sequence 102, App Sequence 102, App Sequence 3964, App Sequence 3776, App Sequence 5533, App Sequence 5533, App Sequence 101, App Sequence 1064, App Sequence 1366, App Sequence 1366, App Sequence 1366, App Sequence 1064, App Seque
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APPLICANT: PETERS, ROBERT T.
APPLICANT: PETERS, ROBERT T.
APPLICANT: PETERS, ADARES M.
APPLICANT: PALCANES M.
APPLICANT: PALCAMELA, VITO J.
APPLICANT: BITONII, ALAN R.
TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945.0003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT APPLICATION NUMBER: 60/468,835
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PALCHIN Ver. 3.2
LENGTH: 36
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US-11-045-024-7039
US-11-045-024-103
US-11-045-024-102
US-11-045-024-3967
US-11-1045-024-3967
US-11-112-277-40
US-11-112-277-39
US-11-045-024-3776
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US-11-045-024-3966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human immunodeficiency virus US-10-841-956A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10841956A Publication No. US20050281829A1 GENERAL INFORMATION: APPLICANT: TAN HEHIR, CRISTINA A.
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APPLICANT: Wilson, Troy E.
APPLICANT: Wilson, Troy E.
APPLICANT: Litzinger, David C.
APPLICANT: Mariani, Roberto
APPLICANT: Kimmel, Bauce E.
APPLICANT: Keefe, William M.
TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
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TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
TITLE OF INVENTION NUMBER: 60/590,035
FRIOR FILING DATE: 2004-07-21
FRIOR FILING DATE: 2004-07-21
FRIOR FILING DATE: 2005-03-07
FRIOR FILING DATE: 2006-03-07
FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 37
; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
90.6%; Score 174; DB 7;
Best Local Similarity 88.9%; Pred. No. 4.3e-16;
Matches 32; Conservative 3; Mismatches 1
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CURRENT APPLICATION NUMBER: US/11/112,277;
CURRENT FILING DATE: 2005-04-22;
PRIOR APPLICATION NUMBER: US 60/565,228
PRIOR FILING DATE: 2004-04-23;
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0;
SEQ ID NO 33
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
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US-11-187-687-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-187-687-24; Sequence 24, Application US/11187687; Publication No. US20060019347A1; GENERAL INFORMATION: APPLICANT: Cho, Ho Sung; APPLICANT: Daniel, Thomas O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: T20 Analogue FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hays, Anna-Maria
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| APPLICANT: Cho, Ho Sung
| APPLICANT: Daniel, Thomas O. |
| APPLICANT: Daniel, Thomas O. |
| APPLICANT: Daniel, Thomas O. |
| APPLICANT: Hays, Anna-Maria |
| APPLICANT: Wilson, Troy E. |
| APPLICANT: Mariani, Roberto |
| APPLICANT
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Sequence 33, Application US/11112277
Publication No. US20050267293A1
GENERAL INFORMATION:
APPLICANT: Bougquet-Gagnon, Nathalie
APPLICANT: Guraishi, Omar
APPLICANT: Bridon, Dominique P.
TITLE OF INVENTION: MSTHOD FOR THE PURIFICATION OF ALBUMIN
TITLE OF INVENTION: CONJUGATES
FILE REFERENCE: 500862003700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 4.2e-16;
3; Mismatches 1;
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ilarity 88.9%; Pred. No. 4.2e-16;
Conservative 3; Mismatches 1.
PRIOR APPLICATION NUMBER: bu, 532, 2017
PRIOR FILING DATE: 2004-01-26
PRIOR PELLONG NUMBER: 60/487, 964
PRIOR FILING DATE: 2003-07-17
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/11187687
Publication No. US20060019347A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9%;
Matches 32; Conservative
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32; Conserv
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Best Local 8
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us-09-809-060a-4.szlm50.rapbn

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APPLICANT: ARNTZEN, Charles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REPERENCE: 01231.000602
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2004.09-03
PRIOR APPLICATION NUMBER: PCT/US03/07073
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
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APPLICANT: BITONTI, ALAN J.
APPLICANT: STATTEL, JAMES
TITLE OF INVENTION: IMMUNOSLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
FILE REFERENCE: 08945.0007-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PETERS, ROBERT T.
APPLICANT: STATTEL, JAMES M.
APPLICANT: SALOMBELLA, VITO J.
APPLICANT: BITONIS.
ITTLE OF INVENTION: PC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 134; DB 6;
Pred. No. 5:3e-11;
0; Mismatches 1;
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Pred. No. 1.4e-10;
4; Mismatches 4
                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
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CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
SOFTWARE: PACENTIN VOS: 59
SOFTWARE: PACENTIN VOI: 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 SQIQQEKNEQELLELDKWASLWNWF 36
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Publication No. US20050281829A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: TAN HEHIR, CRISTINA A.
APPLICANT: MEZO, ADAM R.
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75.0%;
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96.0%;
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Best Local Similarity 75.04
Matches 24, Conservative
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Best Local Similarity 96.0°
Matches 24; Conservative
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APPLICANT:
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                TITLE OF INVENTION: For Fusion Proteins For Enhancing the Immunogenicity of TITLE OF INVENTION: Protein and Peptide Antigens
TITLE OF INVENTION: Protein and Peptide Antigens
FILE REFERENCE: LEX-0.7
CURRENT APPLICATION NUMBER: US/11/089,426
FURNENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: US/09/621,268
PRIOR PILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/144,965
PRIOR FILING DATE: 1999-07-21.
SOFTHARE: PATENTIN DATE: 1299-07-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MOR, Teafrir
APPLICANT: MATOBA, Nobuyuki
APPLICANT: MATOBA, Nobuyuki
APPLICANT: ARNIZER, Charles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.0006U2
CURRENT PELING DATE: 0204-09-03
PRIOR PELICATION NUMBER: PCT/US03/07073
PRIOR PELICATION NUMBER: FCT/US03/07073
PRIOR APPLICATION NUMBER: 60.3462,247
PRIOR FILING DATE: 2002-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
US-10-506-796A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 134; DB 6; Length 35;
Pred. No. 5.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 162; DB 7;
Pred. No. 1.8e-14;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10506796A
Publication No. US20060013831A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.4%;
                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.8%;
96.0%;
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SOFTWARE: PatentIn version 3.2
Wesolowski, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.2
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Conservative
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Best Local Similarity
Matches 24; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-089-426-10
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                                                                                                                                                                                                                                                                    SEQ ID NO 10
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APPLICANT
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Length 36; Indele

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Sequence 5, Application US/10506796A;
Publication No. US20060013831A1
GENERAL INFORMATION:
APPLICANT: MATOBA, Nobuyuki
APPLICANT: MATOBA, Nobuyuki
APPLICANT: ARNTZEN, Charles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.000602
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT PILING DATE: 2004-09-03
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VETSION 3.2
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PAPLICANT: MATORA, NOBUJUKi
APPLICANT: ARANZEN, Charles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: PEPTIDE
; LOCATION: (1)...(36)
; OTHER INFORMATION: HIV-1 isolate 593 clone (residues 649-685)
US-10-506-796A-5
                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(36)
; OTHER INFORMATION: HIV-1 isolate 1924v3.20 (residues 649-685)
US-10-506-796A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.2%; Score 129; DB 6; 92.0%; Pred. No. 2.3e-10; tive 1; Mismatches 1;
  CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: PCT/US03/07073
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 36
TYPE: PRI
ORGANISM: Human immunodeficiency virus type 1
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human immunodeficiency virus type 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92.03
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
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US-10-506-796A-6
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Publication No. US20060013831A1
GENERAL INFORMATION:
APPLICANT: MOR, TSAITIE
APPLICANT: MATCBA, Nobuyuki
APPLICANT: ARMYZEN, Chailes
TITLE OF INVERTION:
FILE REFERENCE: 01231.0006U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sequence 34, Application US/11112277

Publication No. US20050267293A1

GENERAL INPORMATION:

APPLICANT: Bousquet.Gagnon, Nathalie

APPLICANT: Bridon, Dominique P.

TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN

TITLE OF INVENTION: CONJUGATES

FILE REFERENCE: 500862003700

CURRENT APPLICATION NUMBER: US/11/112,277

CURRENT FILING DATE: 2005-04-22

PRIOR APPLICATION NUMBER: US 60/565,228

PRIOR PLING DATE: 2004-04-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PRAESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                          ch 68.2%; Score 131; DB 7; Length 39; Similarity 75.0%; Pred. No. 1.4e-10; 24; Conservative 4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-34
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CURRENT APPLICATION NUMBER: US/11/029,003
CURRENT FILING DATE: 2005-01-05
PRIOR APPLICATION NUMBER: 60/539,207
FRIOR FILING DATE: 2004-01-26
PRIOR FILING DATE: 2003-07-17
PRIOR PLING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/469,600
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN VET: 3.2
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Human immunodeficiency virus US-11-029-003-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: T1249 Analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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US-10-506-796A-7
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NAME/KEY: PEPTIDE:
LOCATION: (1)..(35)
COTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
US-10-506-796A-4
                                                                                                                                                                                                                       NAME/KEY: PEPTIDE
LOCATION: (1)..(36)
NOTHER INFORMATION: HIV-1 isolate 98BRRS012 (residues 649-685)
US-10-506-7966-7966-7
                                                                                                                                                                                                                                                                                                         Query Match 64.6%; Score 124; DB 6; Length 36; Best Local Similarity 88.0%; Pred. No. 1e-09; Matches 22; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%; Score 122; DB 6; Length 36;
88.0%; Pred. No. 1.8e-09;
tive 0; Mismatches 3; Indels
                                                                                                                                                                        TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
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CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2004-09-03
FRIOR APPLICATION NUMBER: PCT/US03/07073
FRIOR FILING DATE: 2003-03-06
FRIOR APPLICATION NUMBER: 60/362,247
FRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                             12 SQIQQEKNEQELLELDKWASLWNWF 36
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Matches 22; Conserva
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completed: March .6, 2006, 15:54:21 ne : 10 secs

Search co Job time

12 SQIQQEKUNEQELLELDKWASLWNWF 36

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OM protein - protein search, using sw model

March Run on:

6, 2006, 16:12:57; Search time 117.333 Seconds (without alignments) 134.809 Million cell updates/sec

US-09-809-060A-4 36

1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36 Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

2443163 segs, 439378781 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

A_Geneseq Database :

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2002s:* geneseqp2001s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aav89840 Core polv	Core	Core	Aab78241 Core poly	Aau70182 HIV virai	Abb01248 Viral DP1	Abb01249 Viral DP1	Abb02833 Viral cor	Aau13794 DP178-lik	Aau13795 DP178-lik	Aao18774 HIV gp41	HΙV	Ade02854 Hybrid po		Peptide		HIV-1	Ady71495 HIV-1 tra	Aay89911 Core poly	2 Core	Abb01319 Viral DP1	Aau13865 DP178-lik	Ade02837 Hybrid po	
SUMMARIES	JD	AAY89840	AAY89841	AAB78242	AAB78241	AAU70182	ABB01248	ABB01249	ABB02833	AAU13794	AAU13795	AA018774	AA018826	ADE02854	ADE02853	ADN06925	ADS87260	ADY71547	ADY71495	AAY89911	AAB78312	ABB01319	AAU13865	ADE02837	AAY22811
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ф	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	4.69	69.4	69.4	69.4	69.4	69.4
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	Result No.	1		Ю	4	'n	9	7	00	6	10	11	12	13	14	15	16		18		20	21	22	23	24

Envelope	Human imm	SEQ ID NO	Envelope	Human imm	Human imm	HIV Env p	Viral cor	DP-178 ho	HIV-1 180	T20/DP178	T20/DP178	Anti-HIV	DP-178 ho	Core poly	HIV-1 180	T20/DP178	T20/DP178	Anti-HIV	Core poly	Viral cor
Abg68282	Abu57689	Aay22825	Abg68296	Abu57703	Adp20072	Adx39685	Abb02834	Aar64384	Aab14657	Aab52674	Aab52699	Aab54921	Aar64385	Aay88708	Aab14658	Aab52698	Aab52675	Aab54922	Aab77063	Abb01532
ABG68282	ABU57689	AAY22825	ABG68296	ABU57703	ADP20072	ADX39685	ABB02834	AAR64384	AAB14657	AAB52674	AAB52699	AAB54921	AAR64385	AAY88708	AAB14658	AAB52698	AAB52675	AAB54922	AAB77063	ABB01532
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52	52	22	52	52	52	25	24	22	22	22	22	22	. 55	22	22	22	22	22	22	22
25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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Envelo 6 69.4 268 6 ABU57889 Abg68295 Abg68295 Bbuss Abg68295 Bbuss Abg68295 Bbuss Bbuss

ALIGNMENTS

AAY89840 standard; peptide; 36 AA. AAY89840; AAY89840

23-MAY-2000 (first entry)

Core polypeptide fragment T No. 1409.

Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; anglogenic factor.

Unidentified

WO9959615-A1.

25-NOV-1999.

99WO-US011219. 20-MAY-1999;

98US-00082279 20-MAY-1998;

(TRIM-) TRIMERIS INC.

Lambert DM; Anwer MK, Merutka G, Guthrie KI, Barney S,

WPI; 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence

Disclosure; Page 45; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (1941) protein sequences, especially from HIV-1. HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or prevention of a disease. The core polypeptides are bloactive peptides selected from a growth factor, cytokine, differentiation factor, interferon, colony stimulating factor, hormone or angiogenic

Pred. No. 4.2e-25;

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The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, pepcially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor. Interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusegenic treatments.
factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAY88651-Y90655 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; angiogenic factor.
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                                                                                                                                                                                                    Gарв
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                                                                                                                                                              Length 36;
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                                                                                                                                                            DB 3; L
4.2e-25;
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                                                                                                                                                        100.0%; Score 36; DB
100.0%; Pred. No. 4.2/
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             AAY89841 standard; peptide; 36
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                                                                                                                                                                                Similarity
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Best Local S
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AAY89841
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DB 3;

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid to properties relative to those exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide and core polypeptides can be used for modulating fusogenic events and intracellular processes involving coil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchanges and sperm-egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus-cell fusion (e.g. viral)
                                                                                                                                                                                                                                                                                                                        Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic; antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections caused by human immunodeficiency virus, respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide.
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100.0%; Pred. ...
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                                                                                                                                                                                   AAB78242 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-2000; 2000WO-US018772.
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                                                                                                                                                                                                                                                       (first entry)
       Similarity 100.
36; Conservative
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                                                                                                                                                                                                                                                                                           Core polypeptide T1410.
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Les 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                       19-APR-2001
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       Best Local
Matches 3
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HIV viral envelope protein stabilising peptide #4.

14-FEB-2002 (first entry)

AAU70182;

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Core polypeptide, enhancer, antiviral, anti-HIV, virucide, hepatotropic, antiinflammatory; hybrid polypeptide, coiled-coil peptide interaction, fusion-related disorder, bacterial infection, viral infection.
                                                                                                                                                                                                                                                                             New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36;
                                                                                                                                                                                                                                           Lambert DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 36; DB 4;
                                                                                                                                                                                                                                           Merutka G, Anwer MK,
                                                                                                                                                                                                                                                                                                                   Disclosure; Page 58; 151pp; English.
                  AAB78241 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      procedure in which they are used
                                                                                                                                                                                     10-JUL-2000; 2000WO-US018772.
                                                                                                                                                                                                      09-JUL-1999; 99US-00350641.
                                                      (first entry)
                                                                       Core polypeptide T1409.
                                                                                                                                                                                                                                          Guthrie KI,
                                                                                                                                                                                                                        (TRIM-) TRIMERIS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36 AA;
                                                                                                                                               WO200103723-A1.
                                                                                                                             Unidentified.
                                                      19-APR-2001
                                                                                                                                                                  18-JAN-2001
                                                                                                                                                                                                                                          Barney S,
                                   AAB78241;
RESULT 4
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The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinnetic properties relative to those exhibited by the core polypertide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide or the hybrid and core polypeptide or be used for modulating fusogenic events and intracellular processes involving coiledcoil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg fusion, intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus-cell fusion (e.g. viral).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and polio virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side effects. In addition, this increases the sensitivity of the diagnostic
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Indels
                 Pred. No. 4.2e-25; Mismatches 0;
                                                              1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
         100.0%; Pred. ....
Query Match 100.
Best Local Similarity 100.
Matches 36; Conservative
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1 YTSLIYSLLEKSQIQQEKORQELLELDKWASLWNWF 36 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF

ABB01248 standard; peptide; 36 AA

RESULT 6 ABB01248

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Gaps ö (revised)
(revised)
(first entry)

11-SEP-2003 06-AUG-2003 03-JAN-2002

ABB01248;

444444

AAU70182 standard; peptide; 36 AA AAU70182 ID AAU7 XX RESULT 5

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The invention relates to methods of generating immunogens that elicit neutralising antibodies which target regions of viral envelope proteins such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-
1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and AAU70677-AAU70173 represent stabilising peptides modelling the alpha-
12 AAU70677-AAU70743 represent stabilising peptides modelling the alpha-
13 CAUTO677-AAU70743 represent stabilising peptides modelling the alpha-
14 CAUTO677-AAU70743 represent stabilising peptides modelling the used as vaccine immunogens. Immunogenic compositions comprise a viral envelope to vaccine immunogenic compositions comprise a viral envelope protein or its fragment exterior to the viral membrane, a stabilising peptide to disrupt formation of structural intermediates necessary for viral fusion and entry, and optionally, a viral cell surface receptor or tis fragment to form a stabilised, fusion active cenvelope protein or its fragment to form a stabilised, fusion active cenvelope. Virus neutralisation assays are used to determine the ability of antibody response raised against HIV1 gp41 domains. The sequences and membrane centering are used to characterise the methods are used in inhibiting HIV1 gp41 domains. The sequences and membrane control in this first of the control of the c
                                                                                                                                                            Human, HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
alpha-helical region; ectodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic composition for inhibiting HIV infection, comprises viral envelope protein or its fragment exterior to viral membrane, a stabilizing peptide, and, optionally, viral cell surface receptor or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PANA-) PANACOS PHARM INC.
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                                                                                                                                                                                                                                                                             Homo sapiens
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Sista P;

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The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-637 (heptad repeat region HR2) and 558-555 (heptad repeat region HR1) respectively, of HIV-ILM1 transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-bUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                           Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
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virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
                                                                                                                                                                                                                                                                                          Lambert DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 36; DB 4; I 100.0%; Pred. No. 4.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                            Antczak JB, Delmedico MK, Erickson JB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 58; 587pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB02833 standard; peptide; 36 AA
                                                                                                                                                                 07-FEB-2001; 2001WO-US003988.
                                                                                                                                                                                                           29-FEB-2000; 2000US-00515965.
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                                                                                                                                                                                                                                                  (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-514829/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164013-A2.
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03-JAN-2002
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infection
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                                       Viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-555 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein 9941. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV septentication. The present sequence is a peptide provided in the specification. (Updated on 06-NUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                        Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
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                                                                                                                                                                                                                               note= "N-terminal is substituted by Ac"
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100.0%; Pred. No. 4.2e-25
tive 0; Mismatches 0
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                 Viral DP178/107-like region peptide T1409
                                                                                                                                                                                                                                                                      /note= "C-terminal amide"
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Matches

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Length 36; Indels

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Sequence 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU13795;
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AAU13795
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                                                                                                                                               The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-555 (heptad repeat region HR1) respectively, of HIV-ILM1 transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides darived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
                                                                               Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41; antifusogenic; antiviral; HIV transmission; mutant; mutein.
                                   Sista P;
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                                   Lambert DM,
                                                                                                                                                                                                                                                                                                                                           4.2e-25;
hes 0;
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Pred. No. 4.2e-25;
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                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                   Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DP178-like/DP107-like peptide T-1409.
                                                                                                                             Disclosure; Page 525; 587pp; English
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100.0%; Pr
tive 0; 1
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                                  Delmedico MK,
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                                                                                                                                                                                                                                                                                                                                                      Conservative
            (TRIM-) TRIMERIS INC.
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Best Local Similarity
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                                                         WPI; 2001-514829/56.
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                                Antczak JB,
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                                                                                                        infection
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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus I (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP107 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention
Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 36; DB 4;
100.0%; Pred. No. 4.2e-25
:ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1; isolate LAI
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                                                                                                                                            Disclosure, Page 77; 259pp; English
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Best Local Similarity 100.0
Matches 36; Conservative
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Mismatches

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The present invention relates to a method of treating an HIV infection in an individual, which involves administering in combination a chemokine co-receptor 5 (CCRE) antagonist or its salt and a DP-178 polypeptide or its derivative. Other viral infections can also be treated using the method. The present sequence is a peptide derived from HIV and useful in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of HIV infection in an individual involves administration of a combination of chemokine co-receptor five antagonist and a specified HIV envelope polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV gp41 protein DP-178 region derived peptide SEQ ID NO:
                                                          1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF
                                                                                               1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF
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                                                                                                                                                                                                                                                                         AAO18826 standard; peptide; 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus
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   Conservative
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36;
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   Matches
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                     DP178-11; The proposition of the contract of the proposition of the contract o
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   invention (AAU12559-AAU14009) comprise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Pred. No. 4.2e-25;
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100.0%; Pr
tive 0;
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Best Local Similarity
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Best Local Similarity
Matches 36; Conserv
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Length 36;
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                                                                                    YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                    4.2e-25;
 100.0%; Score 36; DB 5; 100.0%; Pred. No. 4.2e-25
                                 0; Mismatches
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                                                                                                                                                                                 ADE02854 standard; peptide; 36
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                                 36; Conservative
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ID ADEC
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XX 29-c
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US2004063637-A1
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                                                                                                                                                                                                                                                                   The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WQRWEQKI or WASIWEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel bybrid polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core polypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging tructures in vivo. The core polypeptide and hybrid polypeptides are useful for modulating fusogenic events and exhibit antifusogenic or antiviral activity. The novel hybrid polypeptide is useful for decreasing viral infection and modulating intracellular processes involving coiled-coil peptide interactions. The novel hybrid polypeptide is useful for antiorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also or iseful as a part of prognosis for preventing disorders including fusion events and viral infection that involves cell-cell and/or virus-cell tusion, and for diagnosis and in vivo imaging methods. This sequence
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                                                                                                                                                                                             New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
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                                                                                                                                                Merutka G, Anwer MK, Lambert DM;
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                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 1361; 70pp; English.
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                                                                                              98US-00082279
                                                                        99US-00315304
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                                                                                                                                                Guthrie KI,
                                                                                                                       (TRIM-) TRIMERIS INC.
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Modified-site
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The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WGEWERN The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel whyrid polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core polypeptide, for example, a polypeptide useful for the treatment or pervention of a disease, or an imaging agent useful for imaging structures in vivo. The core polypeptides and hybrid polypeptides are useful for modulating tusogenic events and exhibit antifusogenic or structures in vivo. The novel hybrid polypeptide is useful for decressing viral infection and modulating intracellular processes involving coiledcoil peptide interactions. The novel hybrid polypeptide comprises insular coil peptide interactions. The novel hybrid polypeptide comprises insular coil peptide interactions in the novel hybrid polypeptide comprises insular coil peptide forms of diabetes. The novel hybrid polypeptide is also or its fragment, so the core polypeptide is useful for ameliorating the symptoms of forms of diabetes. The novel hybrid dolypeptide is also or its fragment forms of diabetes. The novel hybrid dolypeptide is also events and viral infection that involves cell-cell and/or virus-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
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/note= "C-terminal amide"
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Best Local Similarity 100.0
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TRIM-) TRIMERIS INC
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The present invention relates to a pharmaceutical composition comprised of polymer admixed with synthetic peptides derived from human immunodeficiency virus (HIV) gp41. The invention is useful in treating HIV infection (preferrably HIV-1) and act as as antiviral agent. The present sequence is a peptide used in the pharmaceutical composition of the invention
                                                                                                                                                                                              Pharmaceutical composition used to treat Human Immunodeficiency Virus comprises solution comprising synthetic peptide (Human Immunodeficiency Virus fusion inhibitor) in mixture with polyol.
                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 40; 36pp; English.
16-SEP-2003; 2003US-00663589.
                                27-SEP-2002; 2002US-0414441P.
                                                                                                                               Heilman D, Di J, Bray B;
                                                                                                                                                                 WPI; 2004-339372/31.
                                                               (HEIL/) HEILMAN D.
(DIJJ/) DI J.
(BRAY/) BRAY B.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 AA;
```

Gaps ; 0

Query Match
100.0%; Score 36; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.2e-25;
Matches 36; Conservative 0; Mismatches 0; Indels

1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

ઠે g Search completed: March 6, 2006, 16:19:05 Job time : 117.333 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March Run on:

6, 2006, 16:19:28; Search time 19 Seconds (without alignments) 182.305 Million cell updates/sec

US-09-809-060A-4

Perfect score:

1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36 Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters: 0 Word size

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES		
Result No.	Score	Ouery Match	Length	DB	ID		Description
	22	61.1	357	5	S21994		envelope protein a
7	22	61.1	357	~	S21996		
m	22	61.1	358	7	\$21998		
4	22	61.1	443	7	C41621		env polyprotein P
ហ	22	61.1	847	~	T09448	•	envelope glycoprot
9	22	61.1	847	7	S13289		env protein - huma
7	22	61.1	851	~	S33985		
80	22	61.1	853	~	S54384 ·		envelope polyprote
6	22	61.1	854	~	S13288		env protein - huma
10	22	61.1	855	٦	VCLJA2		env polyprotein pr
11	22	61.1	855	-	VCLJZR		
12	22	61.1	856	~	VCLJ3W		
13	22	61.1	856	Н	VCLJH3		
14	22	61.1	859	-	VCLJMN		
15	22	61.1		٦	VCLJSC		env polyprotein pr
16	22	61.1	861	П	VCLJLV		
17	19	52.8	357	7	S21992		protein
18	16	44.4	852	7	T12016		envelope glycoprot
19	. 16	44.4	856	н	VCLJVL		env polyprotein pr
20	15	41.7	846	-	VCLJND		
21	15	41.7	852	П	VCLJBR		env polyprotein -
22	15	41.7	. 859	7	T01672		envelope polyprote
23	11	ö		~	A41621		env polyprotein M
24	11	ö		Н	H44001		
25	10	•		~	S22004		protein
56	10	۲.		ď	S22006		
27	10	۲.	9	0	S21990		envelope protein g
28	80	22.2	454	~	B41621		env polyprotein D
29	89	22.2	592	~	T03682		catechol oxidase (

catechol oxidase (catechol oxidase (env polyprotein pr	env polyprotein -	envelope polyprote	envelope polyprote	env protein - huma	protein -	protein -	protein -		protein -	protein -	env protein - huma		env protein - huma	
833540	T07097	VCLJSI	VCLJH4	JU0266	JT0954	S30453	S30451	S30452	S30456	S30457	S30448	S30455	S30459	S30458	S30454	
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965	599	854	898	136	136	151	151	151	151	151	151	151	151	151	151	
22.2	22.2	22.2	22.2	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	
ω	ထ	80	80	7	7	7	7	7	7	7	7	7	۲.	7	7	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

envelope protein gp120/gp41 - human immunodeficiency virus type 1 C;Species: human immunodeficiency virus type 1, HIV-1

A; Variety: isolate 27B
Cybate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S21994; S70421
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
R;Steuler, H.; Storch-Hagenlocher, D.; Wildemann, B.; Hacke, W.
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as A;Reference number: S21990

determin

A Accession: \$21994 A Molecule type: DNA A; Molecule type: DNA A; Fossidues: 1-357 (STEL) A; Cross-references: UNIPROT: Q78118; UNIPARC: UPI0000178606; EMBL: X61355; NID: g60179; PIDN R; Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B. BJDS Res. Hum. Retroviruses 8, 3-5.59, 1992 A; Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr A; Reference number: S70417; MUID: 92144209; PMID: 1736940

A;Status: preliminary

A; Molecule type: DNA

A;Residues: 1.140,'X',142-312,'X',314-357 <STE2> , A;Cross-references: UNIPARC:UPI00000FF05F; EMBL:X61355; NID:g60179 C;Superfamily: type E retrovirus env polyprotein

Gaps ö Length 357; IndelB DB 2; Le 4.6e-14; 61.1%; Sco... 100.0%; Pred. No.... 0; Mismatches Query Match Best Local Similarity 100.0 Matches 22; Conservative

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RESULT 2

envelope protein gpl20/gp41 - human immunodeficiency virus type 1 (patient 27L). C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C; Accession: S70422;

Risteller, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
Affile: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr A;Reference number: \$70417; WUID:92144209; PMID:1736940
A;Accession: \$70422

A; Status: preliminary

A;Residues: 1-357 <ST2> A;Cross-references: UNIPROT:Q78119; UNIPARC:UPI0000104EC6; EMBL:X61356; NID:g60181; PIDN

A, Experimental source: patient 27L A, Note: submitted to the EMBL Data Library, July 1991

09:19:22

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Gaps

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Rio'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A. Mature 348, 69-73, 1990
Mature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c
A;Reference number: S13288; MUID:91043044; PMID:2172833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q75760; UNIPARC:UP1000010C516; EMBL:U63632; NID:g1465777; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T09448
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submit of the EMBL Data Library, July 1996
A;Reference number: Z16673
A;Recession: T09448
A;Statues: preliminary; translated from GB/EMBL/DDBJ
A;Recule type: DNA
A;Residues: 1-847 <PAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               env polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                   envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.1%; Score 22; DB 2; Length 847;
100.0%; Pred. No. 1e-13;
cive 0; Mismatches 0; Indels
                  Length 443;
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C;Superfamily: type E retrovirus env polyprotein
                  DB 2; Le
5.6e-14;
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100.0%; Pred. No. 1e-13;
cive 0; Mismatches 0
61.1%; Sco...
100.0%; Pred. No. ...
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submitted to the EMBL Data Library, November 1991
A;Reference number: 833979
A;Acession: 833985
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Superfamily: type E retrovirus env polyprotein
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cive 0; Mismatches
                                                                                                                                                                             392 QOEKNEQELLELDKWASLWNWF 413
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                                                                                                                                          15 QOEKNEQELLELDKWASLWNWF 36
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            Query Match 61.1%
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Matches 22, Conservative
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A;Molecule type: DNA
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C/Superfamily: type E retrovirus env polyprotein
C/Superfamily: type E retrovirus env polyprotein
C/Superfamily: type E retrovirus env polyprotein; glycoprotein; immunodeficiency; polyprotein-
E/S21/Product: coat protein gp120 (fragment) #status predicted cGP1>
F/252-443/Product: coat protein gp41 (fragment) #status predicted cGP2>
F/424-443/Promain: transmembrane #status predicted cTMN>
F/424-443/Domain: transmembrane #status predicted cTMN>
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A;Residues: 1-358 <STEL>
A;Cross-treferences: UNIPROT:Q78120; UNIPARC:UPI0000178607; EMBL:X61359; NID:g60182; PIDN
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
*Residues: 1-222,'X', 224-358 <STE2>
A;Cross-references: UNIPARC:UPIO0000FE72C; EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PIC
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebra. A;Reference number: S70417; MUID:92144209; PMID:1736940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11235-11240, 1991
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:1763038
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A;Note: this virus was isolated from the mother's sexual partner
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env polyprotein P - human immunodeficiency virus type 1 (fragment)

NyAlternate names: cost polyprotein

NyContains: amino end of cost protein gp41; carboxyl end of cost protein gp120

C;Species: human immunodeficiency virus type 1, HIV-1

A;NOTE: host Homo sapiens (man)

C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: C41621
                                                                                                                                          Gaps
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                                                                                 Length 357;
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                                                                                                                                          Indels
                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-14;
Matches 22; Conservative 0; Mismatches 0;
               C; Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                     153 QQEKNEQELLELDKWASLWNWF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QOEKNEQELLELDKWASLWNWF 175
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A;Molecule type: DNA
A;Residues: 1-443 <BUR>
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A;Molecule type: DNA A;Residues: 1-855 <SAN> :Molecule type: DNA :Residues: 1-855 <SRI> C; Accession: A24774 A; Accession: A03976 Accession: D26192 A; Accession: A24774 셤 g ð ð C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
S;Accession: S13288
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gpl20
A;Reference number: S13288 MUID:91043044; PMID:2172833
A;Accession: S13288
A;Accession: S13288
A;Accession: S13288
A;Accession: Breliminary
A;Molecule type: DNA
A;Residues: 1-854 cobra
A;Cross-references: UNIPROT:Q78582; UNIPROT:Q782502; UNIPROT:090178; UNIFROT:Q78243; UNIFROT A;Residues: 1-851 <CAR> A;Cross-references: UNIPROT:078243; UNIPARC:UPI00011067CD; EMBL:211530; NID:g60192; PIDN C;Superfamily: type E retrovirus env polyprotein A;Cross-references: UNIPROT:P12487; UNIPARC:UP1000012A027; EMBL:M22639; NID:g329377; PID C;Superfamily: type E retrovirus env polyprotein C;Keywords: polyprotein env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2) N,Alternate names: coat polyprotein C,Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C,Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A03976 ö C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004 C;Accession: S5438 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004 C;Accession: S54377 Bubmitted to the EMBL Data Library, July 1989 A;Reference number: S54377 A;Accession: S54384 A;Accession: S54384 Gaps Gaps Gaps ö ö 61.1%; Score 22; DB 2; Length B54; llarity 100.0%; Pred. No. 1e-13; Conservative 0; Mismatches 0; Indels Length 853 Length 851 Query Match 61.1%; Score 22; DB 2; Length 853 Best Local Similarity 100.0%; Pred. No. 1e-13; Matches 22; Conservative 0; Mismatches 0; Indels Indels envelope polyprotein - human immunodeficiency virus type 1 / Match 61.1%; Score 22; DB 2; Local Similarity 100.0%; Pred. No. 1e-13; nes 22; Conservative 0; Mismatches env protein - human immunodeficiency virus type 1 QOEKNEGELLELDKWASLWNWF 670 550 QQEKNEQELLELDKWASLWNWF 671 15 QOEKNEQELLELDKWASLWNWF 36 QQEKNEQELLELDKWASLWNWF 36 15 QQEKNEQELLELDKWASLWNWF 36 A;Molecule type: genomic RNA A;Residues: 1-853 <THE> Local Similarity hes 22; Conserv mRNA A; Molecule type: Query Match Best Local S: Matches 22 12 649 Query Match Best Loc Matches 셤 셤 ð ઠે 엄 ઠે

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Accession: D26192

Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

ene 52, 71-82, 1987

Fittle: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti

Reference number: A26192; MUID:87248097; PMID:3036660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CiSuperfamily: type E retrovirus env polyprotein

CiSuperfamily: type E retrovirus env polyprotein

E:1-19/Domain: signal sequence #status predicted <SIG>

E:20-855/Product: env polyprotein #status predicted <MAT>

E:20-856/Product: exterior membrane glycoprotein #status predicted <EXT>

E:501-855/Product: exterior membrane glycoprotein #status predicted <TWM>

E:501-855/Product: transmembrane glycoprotein #status predicted <TWM>

E:801-855/Product: Lansmembrane glycoprotein #status predicted <TWM>
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A;Title: Identification and characterization of conserved and variable regions in the en
A;Reference number: A24774; MUID:86218077; PMID:2423250
Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh
tience 227, 484-492, 1985
                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: type E retrovirus env polyprotein (5. Keywords ADD), capsid protein; ocat protein; jamunodeficiency; polyprot (5. Keywords ADD), capsid protein; ocat protein; glycoprotein; signal sequence #status predicted <51G>
F; 31-509/Product: exterior membrane glycoprotein #status predicted <FXT>
F; 510-855/Product: transmembrane glycoprotein #status predicted <FXTA>
F; 510-855/Product: transmembrane glycoprotein #status predicted <TMM>
F; 871-129, 140, 158, 184, 190, 200, 244, 265, 292, 298, 304, 344, 341, 358, 364, 388, 394, 400, 408, 445, 458
F; 610, 624, 636, 815/Binding site: carbohydrate (ABN) (covalent) #status predicted
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                                   Science 227, 484-492, 1985
A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)
A;Reference number: A04003; MUID:85090453; PMID:2578227
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N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus Zr-6
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
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3. 16-13;
0; Indels
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Best Local Similarity 100.09
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6, 2006, 16:26:19
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Matches 22; Conservative
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Job time : 19 secs
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VCLJH3

env protein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
NiAlternate names: coat polyprotein
NiAlternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host thome sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03973
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 113, 277-284, 1985
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; MUID:85111123; PMID:2578615
A;Accession: A03973
A;Accession: A03973
A;Residues: 1-856 cRAT-
A;Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K020
C;Genetics:
A;Gene: env
C;Superfamil: signal sequence #status predicted cited
C;Genetics:
A;Gene: env
C;Superfamin: signal sequence #status predicted cited
C;Genetics:
A;Gene: env
C;Superfamin: signal sequence #status predicted cited
C;Genetics: The Signal sequence glycoprotein #status predicted cited
F;1-30/Domain: signal sequence glycoprotein #status predicted cited
F;1-1-816/Product: transmembrane glycoprotein #status predicted cited
F;188,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Banding site: carbohydrate (Asn) (covalent) #status predic
A; Molecule type: DNA
A; Residues: 1-856 <STA>
A; Cross-references: UNIPROT:P31872; UNIPARC:UP1000012A024; GB:K03455; GB:M38432; NID:g19
C; Genetics:
A; Gene: env
A; Gene: env
C; Superfamily: type E retrovirus env polyprotein; transmembrane protein
C; Keywords: coat protein; GJycoprotein; polyprotein; transmembrane protein
C; Keywords: coat protein gJycoprotein; polyprotein; transmembrane protein
F; 1-29/Domain: signal sequence #status predicted <SIG>F; 1-29/Domain: signal sequence #status predicted <GP>F; 1-29/Domain: signal se
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NiAlternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Home sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
R;Gurgo, C:; Guo, H.G.; Franchini, G:; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta Virology 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.1%; Score 22; DB 1; Length 856; 100.0%; Pred. No. 1e-13; cive 0; Mismatches 0; Indels
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.-- 0; Indels
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Matches 22; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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A; Residues: 1-859:<GUR>
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A,Gene: env
C;Superfamily: type B retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote:
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-859/Product: env polyprotein #status predicted <EPP>
F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is the precursor of the polyprotein immunodeficiency virus type 1 (isolate SC)
NyAlternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Accession: B28922
C;Accession: B28922
C;Accession: B28922
C;Accession: B28922
A;Title: Envelope sequence of two new United States HIV-1 isolates.
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
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C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
E;1-29/Domain: signal sequence #status predicted <SIG>
F;30-861/Product: env polyprotein #status predicted <EPP>
F;87,129,135,140,143,159,163,187,199,234,241,262,276,295,301,302,333,340,356,366,396
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100.0%; Pred. No. 1e-13;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                0; Indels
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Pred. No. 1e-13;
                                                                                                                                                                                                                                   100.0%; Prec. ...
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A;Recidues: 1-861 <GUR>
A;Cross-references: UNIPARC:UP10000174A39
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                     656 QQEKNEQELLELDKWASLWNWF 677
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                                                                                                                                                                                                                                                                                                                                              15 QQEKNEQELLELDKWASLWNWF 36
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein March Run on:

6, 2006, 16:13:17; Search time 122 Seconds (without alignments) 208.189 Million cell updates/sec

US-09-809-060A-4

Perfect score:

1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36 Scoring table: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0

2166443 seqs, 705528306 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMERIES		
Result No.	Score	Query Match	Length	DB.	qI	Description	
-	29	80.6	121	5	O6WH74 9HIV1	06wh74 human immun	
~	29	90.6	122	N	Q9EA81 9HIV1	human i	_
٣	29	90.6	122	N	Q9YXQ1 9HIV1	human	
4	27	75.0	122	~	Q6DL64 9HIV1	human	_
Ŋ	27	75.0	128	~	Q6JEV9 9HIV1	Q6jev9 human immun	_
9	27	75.0	145	~	Q7ZC55_9HIV1	human i	_
7	27	75.0	146	7	Q6JFV9 9HIV1	human i	_
8	27		867	~	Q7ZC00_9HIV1	human	_
6	27	75.0	898	7	Q7ZC01_9HIV1	human	_
10	56		126	ď	Q6V908_9HIV1	human	_
11	25	69.4	34	~	Q69893_9HIV1	Q69893 human immun	
12	25	69.4	49	7	Q69895 ⁹ HIV1	Q69895 human immun	_
13	25	69.4	49	~	Q69896 <u></u> 9HIV1	Q69896 human immun	_
14	25		118	~	Q9E5S3_9HIV1	Q9e5s3 human immun	_
15	25		121	7	Q6WH14 9HIV1	Q6wh14 human immun	_
91	25		122	~	Q6WGU9_9HIV1	Q6wgu9 human immun	_
7	25		122	0	Q6WH11_9HIV1	Q6wh11 human immun	_
8	25		122	~	Q6DL06_9HIV1	Q6d106 human immun	_
19	25		122	N	Q6DL34 9HIV1	Q6d134 human immun	_
50	25		122	~	Q6DL40_9HIV1	Q6d140 human immun	_
21	25	69.4		7	Q9EA80_9HIV1	Q9ea80 human immun	_
	25	69.4	125	~	Q6V900_9HIV1	Q6v900 human immun	_
23	25	69.4		7	Q6V8Z3_9HIV1	O6v8z3 human immun	_
	25		142	7	Q6JFE1_9HIV1	Q6jfel human immun	_
25	25		144	7	Q7ZC91_9HIV1	Q7zc91 human immun	_
56	25		144	~	Q6JFJ2 9HIV1	Q6jfj2 human immun	_
27	. 25		724	7	Q9QKH4 9HIV1	Q9qkh4 human immun	_
28	25		m	24	Q5S516_9HIV1	Q58516 human immun	_
29	25		848	Н	ENV HV1JR	P20871 human immun	_
30	25	69.4	848	N	Q6BC22 9HIV1	Q6bc22 human immun	_
31	25	69.4	848	~	Q6TAN0 9HIV1	Q6tan0 human immun	_

1mmun	immun	1mmur	1mmun	1 mmun	1 mmun	1 mmun	1mmur	1 mmun	fmmun	immun	immun	immun	fmmun
human	human	human	human	human	human	human	human	human	human	human	human	human	human
Q6tanl	Q6tan2	074999	079795	Q902h5	041532	089861	069894	069905	069910	06690	Q6wh02	Q6wh53	Q6wh80
Q6TAN1_9HIV1	Q6TAN2 9HIV1	Q74999_9HIV1	Q79795_9HIV1	Q902HS_9HIV1	041532_9HIV1	Q8Q861_9HIV1	Q69894 9HIV1	Q69905 9HIV1	Q69910_9HIV1	Q69909_9HIV1	Q6WH02_9HIV1	Q6WH53 9HIV1	Q6WH80 _9HIV1
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848	848	848	820	852	860	898	34	34	42	49	117	117	117
69.4	69.4	69.4	69.4	69.4	69.4	69.4	61.1	61.1	61.1	61.1	61.1	61.1	61.1
25	25	25	52	52	22	52	22	22	22	22	22	22	22
32	33	34	35	36	37	38	39	40	41	42	43	.44	45

ALIGNMENTS

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PUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;

A Gouvea M.I.F.S., Guimaraes M.A.A. M., De Oliveira F.E.,

A Gouvea M.I.F.S., Guimaraes M.A.A. M., De Oliveira F.E.,

A Magnanini M.M.F., Brindeiro R.M., Tanuri A.;

"Prevalence of human immunodeficiency virus drug resistance mutations

"Prevalence of Pubman immunodeficiency virus drug resistance mutations

and subtypes in drug-naive, infected individuals in the army health

service of Rio de Janairo, Bractil.";

J. Clin. Microbiol. 42:426-430(2004).

EMBL; AV285022; AAQ68085.1; -; Genomic_RNA.

GO; GO:0018031; C:integral to membrane; IEA.

GO; GO:0018031; C:integral to membrane; IEA.

RO; GO:0018031; C:viral envelope; IEA.

RO; GO:001898; P:structural molecule activity; IEA.

R Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                         Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae, Lentivirus, Primate lentivirus group.
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                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.6%; Score 29; DB 2; Le
llarity 100.0%; Pred. No. 6.9e-20;
Conservative 0; Mismatches 0;
   121 AA.
   PRT;
                                                                                                                                                                   Envelope glycoprotein (Fragment)
                                                                                                                                                                                                                              Human immunodeficiency virus 1.
QEWH74 9HIV1 PRELIMINARY;
QEWH74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 29; Conserv
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NON TER 1
NON TER 121
SEQUENCE 121 AA;
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8 LLEKSQIQQEKNEQELLELDKWASLWNWF 36 g à

01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Envelope glycoprotein (Fragment). OPEA81_9HIV1 PRELIMINARY; 09EA81, **09EA81** CSGEPPPP

Name=env; Human immunodeficiency virus 1. Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

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Yang C., Li M., Shi Y.P., Winter J., van Eijk A.M., Ayisi J., Hu D.J., Steketee R., Nahlen B.L., Lal R.B.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AY4931S6; AAT05980.1; -; Genomic_RNA.
                                                                                                                                                                                                                                                                                         Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalish M.L., Robbins K.E., Pieniazek D., Schaefer A., Nzilambi N.,
Quinn T.C., StLouis M.E., Youngpairoj A.S., Phillips J., Jaffe H.W.,
Polks T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Recombinant viruses and early global HIV-1 epidemic.";
Emerg. Infect. Dis. 10:127-1249 (2004).
EMBL, A4667639, AAT74945.1; '; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IFR00328; Env.GP41.
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122 AA; 14800 MW; 862308FF35EB4A3F CRC64;
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128 128
128 AA; 15494 MW; 807346D5EB52C194 CRC64;
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005199; F:structural molecule activity; IEA.

InterPro; IPR000328; Env_GP41.

Pfam; PF00517; GP41; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                             Last sequence update)
Last annotation update)
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ilarity 100.0%; Pred. No. 5.7e-18;
Conservative 0; Mismatches 0;
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                                                                                   122 AA
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                                                                                                                                            Z5-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
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QGJEV9;
                                                                                   QEDL64_9HIV1 PRELIMINARY;
QEDL64;
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                      MEDLINE=20134570; PubMed=10669328; DOI=10.1086/315253; Weidle P.J., Ganea C.B., Irwin K.L., Pieniazek D., McGowan J.P., Weidle P.J., Ganea C.B., Irwin K.L., Pieniazek D., McGowan J.P., Colivo N., Ramones A., Schable C., Lal R.B., Holmberg S.D., Errst J.A.; Presence of human immunodeficiency virus (HIV) type 1, group M. non-B subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic diversity in the United States."; J. Infect. Dis. 181:470-475(2000).

EMBL, AF190971; AAG02333.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanuri A., Swanson P., Devare S., Berro O.J., Savedra A., Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.; "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."; Acquir. Immune Defic. Syndr. Hum. Retrovirol. 20:60-66(1999).
EMBL, AF034052; AACT9304.1; -; Genomic RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 122 122 123 MW; C3FE4DB1F8B5BCBD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005199; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
PF00517; GP41; 1.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00190319; F:erructural molecule activity; IEA.
InterPro; IPRO0328; Env_GP41.
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100.0%; Pred. No. 6.9e-20;
ive 0; Mismatches 0;
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Lentivirus; Primate lentivirus group.
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                                                                                      NUCLEOTIDE SEQUENCE.
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les 29; Conserv
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                          NCBI_TaxID=11676;
                                                                                                                    STRAIN=BX923;
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[1] TOUCLEOTIDE SEQUENCE
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NON TER 146
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Yang C., Li M., Shi Y.P., Winter J., van Eijk A.M., Ayisi J., Hu D.J., Yang C., Li M., Shi Y.P., Lal R.B.;
Steketee R., Nahlen B.L., Lal R.B.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY492806, AY492806, AT05630.1; -; Genomic_RNA.
HSSP; P04578; IR33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Boulne R., Arendt V., Schneider F., Hemmer R., Schnit J.-C. "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
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145 AA; 16928 MW; D72B68F6A0812805 CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005199, F:serructural molecule activity; IEA.
InterPro, IPR000328; Env GP41.
PF00517; GP41; 1.
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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J. Acquir. Immune Defic. Syndr. 33:134-139(2003)
EMBE; AX185465; AAO65740.1; -; Genomic_RNA.
HSSP; P04578; 1DLB.
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                                                                                         95 EKSQIQOEKNEQELLELDKWASLWNWF 121
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                                                             10 EKSQIQQEKNEQELLELDKWASLWNWF 36
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MEDLINE=22679027; Pubmed=12794544;
DOI=10.1097/00126334-200306010-00003;
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Q7ZC55;
   Conservative
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01-OCT-2003
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TO QÓJEVOS 94
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DT 05-J
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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146 AA; 17524 MW; 642595EF4695BE02 CRC64;
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GO:0016021; C:integral to membrane; IEA.
GO:0019031; C:viral envelope; IEA.
GO:0005198; F:structural molecule activity; IEA.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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100.0%; Pred. No. 3.2e-17;
iive 0; Mismatches 0;
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Pred. No. 6.6e-18;
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100.0%; Pred. No. ...
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InterPro; IPR000777; GP120.
GO; GO:0016021; C:integral to
GO; GO:0019031; C:viral envelo
GO; GO:0005198; F:structural m
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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ID Q7ZC01 9HIV1 PRELIMINARY;
AC Q7ZC01; ... 'memmirel, 2.
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Best Local Similarity 100.0
Matches 27; Conservative
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Pfam; PF00517; GP41; 1.
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Name=gp160;
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Name=gp160;
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Lentivirus; Primate lentivirus group
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
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GULL-2003) to the EMBL/Genbank/DDBJ databases.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016031; C:viral envelope; IEA.
GO; GO:005199; F:structural molecule activity; IEA.
PPEODS17; GP41; 1.
Daniels R.S., Wilson P., Patel D., Longhurst H., Patterson S.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
REML; AJ535609; CAD59655.1; -; Genomic_DNA.
RSSP: P04578; 1DLB.
RSSP: P04578; 1DLB.
RSSP: Q72C01; 83-127, 209-504, 552-638.
RSR; Q72C01; 83-127, 209-504, 552-638.
RGC; GO:0016021; C:integral to membrane; IEA.
RGC; GO:0019031; C:viral envelope; IEA.
RITERPRO; IPR000378; ENV.GP41.
RITERPRO; IPR000777; GP120.
RFam; PF00516; GP220; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%; Score 27; DB 2; Length 868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00517; GP41; 1.
AIDS; Envelope protein; Transmembrane.
GRAIFINCE 868 AA; 98437 MW; F563775C680E2348 CRC64;
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Q59893 9HIV1 PRELIMINARY; PRT; 34 AA.

Q69893;

01-NOV-1996 (TYEMBLrel. 01, Created)

01-NOV-1996 (TYEMBLrel. 01, Last sequence update)

G1-JUN-2003 (TYEMBLrel. 24, Last annotation update)

G2941 (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 3.2e-17; ive 0; Mismatches 0;
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Best Local Similarity
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060'908 9HI
1D 060'90
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1D 006
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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                                                 NUCLECTIDE SEQUENCE.
MEDLINE-94211861; PubMed-7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emin E.A.;
"Neutralization of divergent human immunodeficiency virus type 1
"Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
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100.0%; Pred. No. 2e-16;
tive 0; Mismatches 0; Indels
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34 AA; 4196 MW; 0C7CAA60A164BB9C CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
NON TER 1 1
NON TER 34 34
SEQÜENCE 34 AA; 4196 MW; OC7CAA60A164B89C CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0001998; Figuretural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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Last annotation update)
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EMBL, U06723; AAA19136.1; -; mRNA.
HSSP; P31872; 1LB0.
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Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994)
EMBL; UGC725; AAA19138.1; -; mRNA.
HSSP; 931972; 1LBO.
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 100.(
Matches 25; Conservative
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NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
NCBI_TaxID=11676;
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MEDLINE=20414627; PubMed=10957729; DOI=10.1089/08892220050117087;
Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura B.T.,
John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
"Presence of Diverse Human Immunodeficiency Virus Type I Viral
Variants in Cameroon.";
                                                                                                                                                                                                                                                                                                                                                                                          MUCLEOTIDE SEQUENCE.
MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
MEDLINE=94211861; PubMed=7512731;
Medler P.M., Resaler J.A., Bootes L.J., Tung J.S., Arnold B.A., Keller P.M., Shevergent D.A.;
"Neutralization of divergent human immunodeficiency virus type 1 variants and primary isolates by IAM-41-2F5, an anti-gp41 human monoclonal antibody.";
Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
EMBL; U06726; AAA19139.1; -; mRNA.
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GG; GG:0019031; C:viral envelope; IEA.
GG; GG:00190319; F:structural molecule activity; IEA.
Intervo; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                          Q69896 9HIV1 PRELIMINARY;
Q69896;
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Q9E5S3;
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Pubmed-14715797; DOI=10.1128/JCM.42.1.426-430.2004;
Pubmed-14715797; DOI=10.1128/JCM.42.1.426-430.2004;
Pubmed-17. Soares M.A. Speranza F.A.B., Ishlii S.K., Vieira M.C.G.,
Ad Gouvea M.I.F.S., Guimares M.A.A.M., De Oliveira F.B.,
Magnanini M.M.F. Brindeiro R.M., Tanuri A.;
"Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naive, infected individuals in the army health and subtypes in drug-naive, infected individuals in the army health J. Ciin. Microbiol. 42:426-430(2004).

EMBL, AV285082; AAQ68145.1; -; Genomic_RNA.
GO; GO:0015081; C:integral to membrane; IEA.
GO; GO:001598; F:structural molecule activity; IEA.
Refin: PP00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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                                                                                                                                                                                                                                                                                  69.4%; Score 25; DB 2; Length 118; 100.0%; Pred. No. 4.5e-16; Live 0; Mismatches 0; Indels
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118 AA; 14275 MW; 1878D17C292899C0 CRC64;
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SMR; Q9ESS3; 1-101.

GO; GG: 0016621; C:integral to membrane; IEA.

GO; GG: 0019031; C:viral envelope; IEA.

GO; GG: 0005198; F:structural molecule activity; IEA.

InterPro; IRR000328; Env_GP41.

Envelope protein.

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NON_TER 118

SEQÜENCE 118 AA; 14275 MW; 1878D17C292899C0 CRC64
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last seq
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Best Local Similarity 100.0
Matches 25; Conservative
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ID QGWH14 9HIV1 PRELIMINARY;
AC QGWH14;
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6, 2006, 16:25:38; Search time 28.6667 Seconds (without alignments) 103.825 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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36 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36 US-09-809-060A-4 Title: Perfect score: Sequence:

Scoring table: OLIGO

572060 seqs, 82675679 residues Searched:

0

Word size :

Gapop 60.0 , Gapext 60.0

572060 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/backfiles1.pep:* Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	App	Ap	Ap	Ap		Αp	Αp	Ap	Ap	Ap	ppl	Appli	ppl	Ap	Αp	Ap	Αp	Αp	Αp	Appl	Appl	Ap	Αp	ppl	ppl	Appl	App
d	240,	1360,	1360,	1360,	1360,	1360,	1360,	1986,	1749,	1938,	10, 4	7, AE	21, A	1361,	1361,	1361,	1361,	1361,	1361,	61, A	61, A	1674,	1704,	53, A		62, A	237,
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}	-223B-24	279B	304B	-784-1360	965A	641C	841A	965A	641C	350-841A-19	-921-1	-056-7	-950	279B	304B	-784-1361	965A	641C	841A	028-	-616-61	965A	-841A	305-	305-	028-	223B
	484-	09-082-	315	834	-515-	-350-	-320-8	-515-	-350-	-350-	570	-596-80	08-965-056-21	-082-	9-315-	09-834-	515	-350-	-350-	08-073-028-61	554	-515-	-350-	0-005-305-5	0-005-305-7	-08-073-028-6	08-484-223B-2
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& Query Match	100	100	100	100	100.0	700	100	69	9	9	9	9	9	9	9	9	9	9	9	9	9	6	9	6	9	9	9
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Sequence 62, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 1675, Appl Sequence 1705, Appl Sequence 237, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl Sequence 790, Appl S
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US-08-554-616-62 US-09-082-279B-59 US-09-013-304B-59 US-09-315-304B-59 US-09-315-965A-59 US-09-515-965A-59 US-09-350-641C-59 US-09-350-641C-59 US-09-350-841A-1705 US-09-350-841A-1705 US-09-350-841A-1705 US-08-360-841A-1705 US-08-360-841A-1705 US-08-360-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-380-841A-1705 US-08-08-380-841A-1705 US-08-08-380-841A-1705 US-09-08-380-841A-1705 US
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ALIGNMENTS

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APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALF: 1.023-2.1.
COMPUTER READ-BLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
Sequence 240, Application US/08484223B Patent No. 6020459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A. 72
REGISTATION UNDRER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
                                                               Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 240:
                                                                                                                                                                Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-484-223B-240
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
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: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10036-2711
                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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100.0%; Score 36; DB 2; Length 36;

Query Match

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US-09-515-965A-1360

i Sequence 1360, Application US/09515965A

j Sequence 1360, Application US/09515965A

j Patent No. 6623741

j GENERAL INFORMATION:

APPLICANT: Anczak, J.

APPLICANT: Lambert, D.

APPLICANT: Lambert, D.

APPLICANT: Lambert, D.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION

TITLE OF INVENTION: WUMBER: US/09/515,965A

CURRENT FILING DATE: 1999-05-29

PRIOR FILING DATE: 1999-05-20

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTHANS

LENGTH: 36

LENGTH: 36

LENGTH: 36
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                                                                                                                                                                                                                                           APPLICANT: Buther, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REPERENCE: 7812-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1360
LENGTH: 36
                                 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0;
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100.0%; Score 36; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                        Sequence 1360, Application US/09834784
Patent No. 6562787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Core polypeptide US-09-834-784-1360
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Mearucka, G.
APPLICANT: Mearucka, G.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACCKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: 09/09/315,304B
CURRENT PILING DATE: 1999-05-20
FRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 136
                               Gaps
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Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservațive 0; Mismatches 0; Indels
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                               Indela
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCHILKA, Gene
APPLICANT: MCHILKA, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REPERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT APPLICATION NUMBER: US/09/082,279B
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1360
LENGTH: 36
100.0%; Pred. No. 2.8e-26; tive 0; Mismatches 0;
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100.0%; Score 36; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                    1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                   Sequence 1360, Application US/09082279B Patent No. 6258782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1360, Application US/09315304B Patent No. 6348568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Core polypeptide
US-09-082-2798-1360
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ORGANISM: Artificial Sequence
                       36; Conservative
                                                                                                                                                                                                                                                                                                                         APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
  Best Local Similarity
                                                                                                                                                                                                                         US-09-082-279B-1360
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APPLICANT: Deliment. ...
APPLICANT: Bricken, J.
APPLICANT: Bricken, J.
APPLICANT: Bricken, J.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: 080/915,965A
CURRENT APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Arwer, M.
APPLICANT: Arwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRE DESCRIPTION: HYBRE DESCRIPTION: HYBRE DESCRIPTION NUMBER: U9/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1749
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100.0%; Pred. No. 3e-16;
tive 0; Mismatches 0;
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3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.4%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 3e-Matches 25; Conservative 0; Mismatches
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                                           Sequence 1986, Application US/09515965A Patent No. 6623741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Core polypeptide US-09-515-965A-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                             APPLICANT: Lambert, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYBEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYBEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBREST US/09/350,641C
CURRENT APPLICATION NUMBER: US/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NO 1360
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Sequence 1360, Application US/09350841A

Patent No. 6750008

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILE REFERENCE: 7872-066-999

CURRENT APPLICATION NUMBER: US/09/350,841A

CURRENT PILLING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 1946

SEQ ID NO 1360

LENGTH: 36
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nilarity 100.0%; Pred. No. 2.8e-26;
Conservative 0: Minner
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                                                                                                                                                                  Sequence 1360, Application US/09350641C Patent No. 6656906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Core polypeptide US-09-350-641C-1360
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Best Local Similarity
Matches 36; Conserva
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Best Local Similarity
Matches 36; Conserva
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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                                                          US-09-350-841A-1938

Sequence 1938, Application US/09350841A

Sequence 1938, Application US/09350841A

Patent No. 6750008

GENERAL INFORMATION:

TOTAL INFORMATION:

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

FILE REPERENCE: 7872-066-999

CURRENT APPLICATION NUMBER: US/09/350,841A

CURRENT FILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 1946

SOFTWARE: PATENTIN VEY: 2.1

SEQ ID NO 1938

LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.4%; Score 25; DB 2; Length 36; Best Local Similarity 100.0%; Pred. No. 3e-16; Matches 25; Conservative 0; Mismatches 0; Indels
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12 SQIQQEKNEQELLELDKWASLWNWF 36
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Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew G. Braisted
APPLICANT: T. Kevin Judice
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 25; Conservative
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ORGANISM: Human
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Sequence 21, Application US/08965056;
Sequence 21, Application US/08965056;
Batent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: James A. Starovasnik
APPLICANT: James A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
APPLICANT: J. Christopher Phelan
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
ADDRESSEE: Genentech, Inc.
STREET: J. DAN WAY
CITY: South San Francisco
STRATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUW TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: WinfPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFTATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFTATION NUMBER: 36,700
REFIERENCE/DOCKET NUMBER: 91005R2
TELEPONMUNICATION INFORMATION:
TELEPHONE: 650/252-8674
TREEDOMMUNICATION INFORMATION:
TELEPHONE: 650/252-8674
INFORMATION FOR SEG ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TURENT AND ACIDS A
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Amino Acid
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Sequence 1161, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Barney, Shawn

APPLICANT: Barney, Shawn

APPLICANT: Anwer, Mohmed

APPLICANT: Anwer, Mohmed

APPLICANT: Anwer, Mohmed

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

TITLE REPERENCE: 7972-043

FILE REFERENCE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FeatSEQ for Windows Version 3.0

SEQ ID NO 1361

LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 SQIQQEKNEQELLELDKWASLWNWF 204
                                                                               ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, PhD., Timochy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELEPHONE: 650/225-8674
TELEPHONE: 650/292-9831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 SQIQQEKNEQELLELDKWASLWNWF 36
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                    APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1361
                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                   LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 24; Conservative
CURRENT APPLICATION DATA:
                                           FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-315-304B-1361
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

March Run on:

6, 2006, 16:26:33 ; Search time 97:3333 Seconds (without alignments) 154.540 Million cell updates/sec

US-09-809-060A-4 36 Title: Perfect score:

1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36 Sequence:

Gapop 60.0 , Gapext 60.0 OLIGO Scoring table:

1867569 segs, 417829326 residues Searched:

0

Word size :

1867569 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB & Maximum DB &

Post-processing: Listing first 45 summaries

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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.ppp:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.ppp:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
/cgn2_6/ptodata/1/pubpaa/US110B_PUBCOMB.ppp:* Published_Applications_AA_Main:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTES

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	. QI	Description
	36	100.0	36		US-09-809-060-4	Sequence 4, Appli
7	36	100.0	36	4	US-10-351-641-1360	
e	36	100.0	36	4	663-	
4	.36	100.0	36	4	US-10-671-282-40	40,
Ŋ	36	100.0	36	ß		5, 1
9	36	100.0	36	Ŋ	US-10-168-295-57	57
7	25	69.4	36	4	US-10-351-641-1749	1749
80	25	69.4	268	٣	US-09-854-816-7	7
6	25	69.4		٣	US-09-854-816-21	21,
10	24	66.7	3	4	US-10-351-641-1361	1361
11	22	61.1	22	4	US-10-005-305-53	
12	. 22	61.1	22	4	US-10-005-305-78	78,
13	22	61.1	22	ഗ	US-10-950-010-130	130,
14	22	61.1	23	4	US-10-351-641-59	26,
15	22	61.1	23	4	US-10-005-305-54	54,
16	22	61.1	23	4	US-10-005-305-77	Sequence 77, Appl
17	22	61.1	23	4	US-10-267-682-237	237,
18	22	61.1	23	4	US-10-267-748-237	237,
19	. 22	61.1	23	'n	US-10-168-295-54	54, 7
20	22	61.1	23	ß	US-10-950-010-129	129,
21	22	61.1	24	4	US-10-351-641-789	789,
22	22	61.1	24	4	US-10-351-641-790	790,
23	22	61.1	24	4	US-10-005-305-55	55,
24	22	61.1	24	4	US-10-005-305-76	76,
25	22	61.1	24	4	US-10-005-305-201	201,
56	22	61.1	24	4	US-10-677-807-236	236,
27	22	61.1	24	'n	US-10-950-010-128	128.

APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR PAPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304

Sequence 7, Applisequence 56, Appl Sequence 12, Appl Sequence 127, Appl Sequence 60, Appl Sequence 236, Appl Sequence 236, Appl Sequence 236, Appl Sequence 126, Appl Sequence 127, Appl Sequence 127, Appl Sequence 125, Appl Sequence 125, Appl Sequence 127, Appl Sequence 124, Appl Sequence 125, Appl Sequence 124, Appl Sequence 135, Appl
US-10-893-551-7 US-10-005-305-56 US-10-005-305-75 US-10-950-010-127 US-10-351-641-60 US-10-005-305-57 US-10-005-305-57 US-10-267-682-236 US-10-267-682-236 US-10-267-682-236 US-10-267-748-236 US-10-950-010-128 US-10-950-010-128 US-10-005-305-59 US-10-005-305-59 US-10-005-305-72 US-10-005-305-72 US-10-005-305-72 US-10-005-305-72 US-10-005-305-72 US-10-950-010-128
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8000126444444 800012645966696969

ALIGNMENTS

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APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
TITLE OF INVENTION: Neutralizing Antibodies Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
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100.0%; Score 36; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YISLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1360, Application US/10351641; Publication No. US20030186874A1; GENERAL INFORMATION:
                   ; Sequence 4, Application US/09809060; Publication No. US20020010317A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Guthrie, K. APPLICANT: Merutka, G. APPLICANT: Anwer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barney, S.
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US-09-809-060-4
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TITLE OF INVENTION: Combination Method For Treating Viral Infections
FILE REFERENCE: INOIS8

CURRENT APPLICATION NUMBER: US/10/168,295

CURRENT FILING DATE: 2002-06-19

PRIOR PELING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

NUMBER: OF SEQ ID NOS: 60/256,657

PRIOR FILING DATE: 2000-12-19

SOFTWARE: PatentIn version 3.1

SEQ ID NO S: 62

LENGTH: 36
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TITLE OF INVENTION: Combination Method For Treating Viral Infections
FILE REFERENCE: INO1358
CURRENT APPLICATION NUMBER: US/10/168,295
CURRENT FILING DATE: 2002-06-19
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 57
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                                                                                               Score 36; DB 4; I
Pred. No. 2.1e-26;
; Mismatches 0;
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100.0%; Score 36; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                              1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Human immunodeficiency virus type 1 US-10-168-295-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human immunodeficiency virus type 1
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                                                                                                                                                                                                                                                                                                                                 US-10-168-295-5
; Sequence 5, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
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0
                            ), OTHER INFORMATION: synthesized US-10-671-282-40
                                                                                                   100.0%;
ilarity 100.0%;
Conservative 0
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Matches 36, Conservative
                                                                                               Query Match
Best Local Similarity
Matches 36; Conserv
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           FEATURE
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TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and TITLE OF INVENTION: their use in therapy
FILE REFERENCE: TRN-004
CURRENT APPLICATION NUMBER: US/10/671,282
CURRENT APPLICATION NUMBER: 60/414,439
PRIOR APPLICATION NUMBER: 60/414,439
PRIOR APPLICATION NUMBER: 00/414,439
PRIOR PILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 40
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaccutical composition for improved administration of HIV TITLE OF INVENTION: Byal-derived peptides, and its use in therapy FILE OF INVENTION : gg-1-derived peptides, and its use in therapy CURRENT FILE OF INVENTION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2
SEQ ID NO 40
LENGTH: 36
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                                                                                                                                                                                                                                                                                                              Length 36;
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2.1e-26;
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100.0%; Score 36; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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100.0%; Pred. No. 2.1
tive 0; Mismatches
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1360
LENGTH: 36
                                                                                                                                                                                                                                      ) OTHER INFORMATION: Core polypeptide US-10-351-641-1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40, Application US/10663589 Publication No. US20040063637A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 40, Application US/10671282; Publication No. US20040122214A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: synthesized US-10-663-589-40
                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-671-282-40
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08/965,056

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12 SQIQQEKNEQELLEI
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                                                                                                                                                                            US-09-854-816-7
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                                                              APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       James A. Wells IIILE OF INVENTION: Constrained Helical Peptides and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUPLING SIP: 94080
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.4%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 3.6 Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
                                                                                                                         FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR PELING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1757 . SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 SQIQQEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQIQQEKNEQELLELDKWASLWNWF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Making Same
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; OTHER INFORMATION: Core polypeptide
US-10-351-641-1749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 DNA
Guthrie, K.
Merutka, G.
                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-854-816-7
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                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Gaps
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TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
                                                                                                                                                                                                                                                                                                                                           Length 268;
                                                                                                                                                                                                                                                                                                                                                                                          Indele
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timochy E.
REGISTRATION NUMBER: 95,700
REPERBNCE/DOCKET NUMBER: P1005R2
               Torchia, PhD., Timothy E. TRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 21
                                                                                                                                                                                                                                        TOPOLOGY: Linear
MOLECULE TYPE: HIV-JRCSF
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 SQIQQEKNEQELLELDKWASLWNWF 203
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Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco STATE: California
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Patent No. US20020151473A1
GENERAL INFORMATION:
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                                                            REFERENCE/DOCKET NUMBER TELECOMMUNICATION INFORMATIO TELEPHONE: 650/225-8674
                                                                                                                                                                                             LENGTH: 268 amino acids
TYPE: Amino Acid
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                  69.4%; £
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                                                                                                                              TELEFAX: 650/952-988
                                             REGISTRATION NUMBER:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7
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Best Local Similarity 100.(
Matches 25; Conservative
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ORGANISM: Artificial Sequence
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APPLICANT: Gathrie, K.
APPLICANT: Anwert, M.
APPLICANT: Anwert, M.
APPLICANT: Anwert, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
FILE REFERENCE: 7872-100
FILE REFERENCE: 7872-100
FILE REFERENCE: 7892-01-24
FRICH APPLICATION NUMBER: 09/351,641
FRICH FILING DATE: 1999-05-20
FRIOR FILING DATE: 1999-05-20
FRIOR PRICH APPLICATION NUMBER: 09/315,304
FRIOR FILING DATE: 1999-05-20
FRIOR APPLICATION NUMBER: 09/082,279
FRIOR APPLICATION NUMBER: 09/082,279
FRIOR FILING DATE: 1999-05-20
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
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                                                                            Length 269;
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3.3e-15;
hes 0; Indels
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                                                                            Query Match 69.4%; Score 25; DB 3; Ler
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                     180 SQIQQEKNEQELLELDKWASLWNWF 204
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Value 10:10-13:10-13:01
Value 13:10-13:01
Value 13:10-13
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; OTHER INFORMATION: Core polypeptide
US-10-351-641-1361
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US-09-854-816-21
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RESULT 12
US-10-005-305-78
Sequence 78, Application US/10005305
Publication No. US2003020341A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHACOCYTE
TITLE OF INVENTION: OF HUMAN PHACOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US0/12371
PRIOR FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR PLING DATE: 1999-05-05
SEQ ID NOS: 203
SOCTHARE: PSSESEQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 22
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; Sequence 130, Application US/10950010
; Publication No. US20050070475A1
; GERRAL INFORMATION:
    APPLICANT: BUIDON, Dominique P.
; APPLICANT: BUDDUELLAB, Nissab
; APPLICANT: BOUDUELLAB, Nissab
; APPLICANT: MILNER, Peter G.
; TITLE OF INVENTION: LOWE LASTING FUSION PEPTIDE INHIBITORS OF VIRAL; TITLE OF INVENTION: LOWG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL; TITLE OF INVENTION: LOWG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL; TITLE OF INVENTION: LOWGER: US/10/950,010
; FILE REPERENCE: 500662001501/REDC-1512
; CURRENT FILING DATE: 2004-09-05
; PRIOR APPLICATION NUMBER: US 60/13451
; PRIOR PILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/134,406
; PRIOR PILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,406
; PRIOR PILING DATE: 1999-05-17
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                                                                                                                Query Match 61.1%; Score 22; DB 4; Length 22; Best Local Similarity 100.0%; Pred. No. 1.6e-13; Matches 22; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Artificial Peptide
US-10-005-305-53
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                                                                                                                                                                                                                                                     15 QQEKNEQELLELDKWASLWNWF 36
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US-10-05-3165-54
Sequence 54, Application US/10005305
Sequence 54, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the TITLE OF INVENTION: T20/DB178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: PORMYL PEPTIDE RECEPTORS
TITLE REFERENCE: NIH171 0012;
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
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Fublication No. US20030186874A1

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Anwer, M.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: PROPERTIES

TITLE OF INVENTION: PROPERTIES

TITLE OF ILLY APPLICANT: OG 3-01-24

FILE REFERENCE: 7872-100

CURRENT APPLICATION NUMBER: 09/351,641

CURRENT APPLICATION NUMBER: 09/350,641

FRIOR APPLICATION NUMBER: 09/315,304

PRIOR PILING DATE: 1999-05-20

FRIOR FILING DATE: 1999-05-20

FRIOR FILING DATE: 1998-05-20

FRIOR FILING DATE: 1998-05-20
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NUMBER OF SEQ ID NOS: 545

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 130

LENGTH: 22

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-950-010-130
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61.1%; Score 22; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         61.1%; Score 22; DB 5; Length 22, 100.0%; Pred. No. 1.6e-13; tive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 23
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Best Local Similarity 100.0
Matches 22, Conservative
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US-10-351-641-59
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Sequence 1, Application US/10841956A
Publication No US20050281829A1
GENERAL INPORMATION:
APPLICANT: TAN HEHR, CRISTINA A.
APPLICANT: MEZO, ADAM R.
APPLICANT: STATTEL, JAMES M.
APPLICANT: STATTEL, JAMES M.
APPLICANT: BALOMBELLA, VITO J.
APPLICANT: BALOMBELLA, VITO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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US-10-841-956A-1
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TYPE: PRT
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Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 22, Appli
Sequence 33, Appl
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                                                                                6, 2006, 16:28:08; Search time 10.3333 Seconds (without alignments) 69.679 Million cell updates/sec
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Sequence
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1: /cgn2_6/ptodata//pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/NSO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                           1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
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US-11-187-687-22

US-11-187-687-24

US-11-089-426-10

US-11-089-426-10

US-10-084-1956A-9

US-10-841-956A-9

US-10-053-100-36

US-11-053-100-38
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                                                                                                                                                                                                                        135346 segs, 20000420 residues
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                                                            protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                           OM protein
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                                                                                                                                                                                                                        Searched:
                                                                                     Run on:
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Result No.

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Sequence 1, Application US/10506796A
FUBLICATION NO. US20060013831A1
GENERAL INFORMATION:
APPLICANT: WOR, TSAFTIC
APPLICANT: MATOBA, Nobuyuki
APPLICANT: ARNTZEN, Charles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.0006U2
CURRENT FILING DATE: 2004-09-03
FRIOR PELICATION NUMBER: BCT/US03/07073
FRIOR FILING DATE: 2003-03-06
FRIOR APPLICATION NUMBER: 60/362,247
FRIOR APPLICATION NUMBER: 60/362,247
FRIOR APPLICATION NUMBER: 60/362,247
FRIOR APPLICATION NUMBER: 60/362,247
FRIOR APPLICATION NUMBER: 012302-03-06
FRIOR SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
FROUR DATE: 2002-03-06
FROUR DA
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37, Appli
39, Appli
31, Appli
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NAME/KEY: PEPTIDE
LOCATION: (1)..(35)
COTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685).
US-10-506-796A-1
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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US-11-053-100-38
US-11-053-100-32
US-11-053-100-35
US-11-042-988-13
US-11-042-988-13
US-11-045-024-13381
US-11-048-42A-37
US-11-014-842A-39
US-11-014-842A-39
US-11-014-842A-31
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US-11-029-003-1
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APPLICANT: MOR, TEafrir
APPLICANT: MATCHA, NObuyuki
APPLICANT: MATCHA, NObuyuki
APPLICANT: MATCHA, NObuyuki
APPLICANT: MATCHA, NObuyuki
APPLICANT: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
TILE REFERENCE: 01231.0006u2
CURRENT FAPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: 60/362,247
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOOTWARE: Patentin version 3.2
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| Sequence 1, Application US/11029003
| Publication No. US20050260194A1
| GENERAL INPORMATION:
| APPLICANT: PETERS, ROBERT T.
| APPLICANT: RIVERA, DANIEL S.
| APPLICANT: BITONI, ALAN J.
| APPLICANT: STATTEL, JAMES
| TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
| FILE REFERENCE: 08945.0007-01000
| CURRENT APPLICATION NUMBER: US/11/029,003
| PRIOR APPLICATION NUMBER: 06/539,207
| PRIOR APPLICATION NUMBER: 60/487,964
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TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945.0003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 1: 36
LENGTH: 36
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                                                                                                                                                                                                                                                                                                          ch 61.1%; Score 22; DB 6; Length 36; 1 Similarity 100.0%; Pred. No. 2.8e-15; 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Human immunodeficiency virus
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Best Local Similarity 100.0
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Matches 22; Conserv
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US-10-506-796A-3
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US-11-029-003-1
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Sequence 22, Application US/11187687
Publication No. US20060019347A1
GENERAL INFORMATION:
APPLICANT: Cho, Ho Sung
APPLICANT: Daniel, Thomas O.
APPLICANT: Haye, Anna-Maria
APPLICANT: Milson, Troy E.
APPLICANT: Mariani, Roberto
APPLICANT: Kamel, Bruce E.
APPLICANT: Keefe, William M.
TITLE OF INVENTION: Acids
TITLE OF INVENTION: Acids
FILE REFERENCE: AMEX-0041.00US
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APPLICANT: Burden, Omar
APPLICANT: Quraishi, Omar
APPLICANT: Bridon, Dominique P.
TITLE OF INVENTION: METHOD FOR THE FURIFICATION OF ALBUMIN
TITLE OF INVENTION: CONJUGATES
FILE REPERBNCE: 500862003700
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/565,228
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Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 22; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.8e-15;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: 60/590,035
PRIOR FILING DATE: 2004-07-21
PRIOR PLING DATE: 2005-03-07
PRIOR PLING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
                                                                                                                                                                           TYPE: PRT ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-22
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/469,600
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 1
LENGTH: 36
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Best Local Similarity 100.
Matches 22; Conservative
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STRANDEDNESS: <Unknown>
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GENERAL INFORMATION:
APPLICANT: Gillies, Stephen D.
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
TITLE OF INVENTION: Proteins For Enhancing the Immunogenicity of
TITLE OF INVENTION: Protein and Peptide Antigens
TITLE OF INVENTION: Protein and Peptide Antigens
FILE REPRENCE: LEX-007
CURRENT PILLION: DATE: 2005-03-24
CURRENT PILLION DATE: 2005-07-21
FRIOR APPLICATION NUMBER: US 60/144,965
FRIOR APPLICATION NUMBER: US 60/144,965
FRIOR PEDICATION NUMBER: US 60/144,965
FRIOR PEDICATION NUMBER: US 60/144,965
SPROFFWARE: PARCHING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 22
SSOFTWARE: PARCHING VEY: 2.0
SSOFTWARE: PARCHING VEY: 2.0
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US-11-089-426-10
                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.1%; Score 22; DB 7; Length 37; Best Local Similarity 100.0%; Pred. No. 2.8e-15; Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                           NAME/KEY: MOD_RES
LOCATION: 37
OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
                       NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 37
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Publication No. US20060019347A1
                                                                                                                                                                                               OTHER INFORMATION: T20 Analogue
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APPLICANT: Cho, Ho Sung.
APPLICANT: Daniel, Thomas O.
APPLICANT: Haye, Anna-Maria
APPLICANT: Wilson, Troy E.
APPLICANT: Litzinger, David C.
                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
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Wilson, Troy E.
Litzinger, David
PRIOR FILING DATE: 2004-04-23
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Kimmel, Bruce E.
                                                                                                                                                                                                                                                                                                                        US-11-112-277-33
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                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                         PEATURE:
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AFFILCANI: NetLe, WILLIAGH
TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
TITLE OF INVENTION: Acids
FILE REFERENCE: Acids
FILE REFERENCE: Acids
FILE REPERENCE: Acids
CURRENT APPLICATION NUMBER: US/11/187,687
CURRENT APPLICATION NUMBER: US/590,035
PRIOR FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: 60/590,709
PRIOR FILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/084,858
FILING DATE: 21-Max-2005
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: US/10/000,321
FILING DATE: 04-Dec-2001
APPLICATION NUMBER: 09/131,551
FILING DATE: «Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 44;
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Publication No. US20050271678A1
GENERAL INFORMATION:
GENERAL MAPP, Stefan
GERERAR, Manfred
GURERTLER, Lutz
TITLE OF INVENTION: Peptides derived from a retro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31, 298
REFERENCE/DOCKET NUMBER: 58315/106/BEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 QOEKNEQELLELDKWASLWNWF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 QOEKNEQELLELDKWASLWNWF 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.1%;
Best Local Similarity 100.0%;
Matches 22; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
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Gaps

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Peptide
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-841-956A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10841956A

Sequence 8, Application US/10841956A

Publication No. US2050281829A1

GENERAL INFORMATION:

APPLICANT: TAN HEHIR, CRISTINA A.

APPLICANT: PETERS, DOBERT T.

APPLICANT: STATTEL, JAMES M.

APPLICANT: BITONTI, JAMES M.

APPLICANT: BITONTI, ALAN R.

TITLE OF INVENTION: FC CHIMBERIC PROTEINS WITH ANTI-HIV DRUGS

FILE REPERENCE: 08945.0003-0000

CURRENT APPLICATION NUMBER: US/10/841,956A

CURRENT FILING DATE: 2004-05-06

PRIOR PILING DATE: 2003-05-06

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PATENTIN VET. 3.2

SEG ID NOS 8

LENGTH. ACC SECOND 
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Sequence 5, Application US/10841956A.

Publication No. US2005031829A1

GENERAL INFORMATION:

APPLICANT: TAN HEHR, CRISTINA A.

APPLICANT: PETERS, ROBERT T.

APPLICANT: PALOMBELLA, VITO J.

APPLICANT: BITONTI, ALAN R.

TILLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-H.:V DRUGS FILE REFERENCE: 08945, 0003-00000

CURRENT APPLICATION NUMBER: US/10/841,956A

CURRENT APPLICATION NUMBER: 06/468,835

PRIOR APPLICATION NUMBER: 60/468,835

PRIOR PILING DATE: 2003-05-06

WINDER OF SEQ ID NOS: 59
                                                                                                                              Length 267;
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61.1%; Score 22; DB 6; Lenyth 269
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 22; Conservative 0; Mismatches 0; Endels
                                                                                                                              DB 6; Le
                                                                                                                              Query Match 61.1%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     246 QÓEKNEQELLELDKWASLWNWF 267
                                                                                                                                                                                                                                                                                                               15 QQEKNEQELLELDKWASLWNWF 36
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ORGANISM: Artificial Sequence
FEATURE: Peptide
; OTHER INFORMATION: construct
US-10-841-956A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 5
LENGTH: 270
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US-10-506-796A-9
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APPLICANT: MARCHA, Nobuyuki
APPLICANT: MATCHA, Nobuyuki
APPLICANT: MATCHA, Nobuyuki
APPLICANT: MARTCHA, Nobuyuki
APPLICANT: MARTCHA, Nobuyuki
APPLICANT: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
TITLE OF INTENTION: 000002
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2004-09-03
PRIOR PILING DATE: 2003-03-06
PRIOR PILING DATE: 2002-03-06
PRIOR PILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATCHIN VERSION 3.2
SEQ ID NO 9
                                                                                                                                                                                                                                                                           Gaps
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| Sequence 4, Application US2080281829A1
| Publication No. US2080281829A1
| GENERAL INFORMATION:
| APPLICANT: TAN HEHIR, CRISTINA A. |
| APPLICANT: MEZO, ADAM R. |
| APPLICANT: PALOMBELLA, VITO J. |
| APPLICANT: PALOMBERIE, 0003-00000
| CURRENT FILING DATE: 2004-05-06 |
| FILE REFERENCE: 08945.0003-00000 |
| CURRENT FILING DATE: 2004-05-06 |
| PRIOR FILING DATE: 2003-05-06 |
| NUMBER OF SEQ ID NOS: 59 |
| SEQ ID NO 4 |
| LENGTH: 267 |
| LENGTH
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                                                                                                                                                                       61.1%; Score 22; DB 7; Length 145; 100.0%; Pred. No. 1.1e-14; tive 0; Mismatches 0; Indels
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    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                  120 QQEKNEQELLELDKWASLWNWF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 QQEKNEQELLELDKWASLWNWF 154
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Best Local Similarity 100.0
Watches 22; Conservative
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tes 22; Conserv
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                                                                                     US-11-084-858-11
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: construct US-10-841-956A-5
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TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS FILE REFERENCE: 08945.5003-00000
CURRENT APPLICATION NUMBER: US/10/841,956A
CURRENT FILING DATE: 2004-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BITONTI, ALAN R.
TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
FILE REFERENCE: 08945.0003-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.1%; Score 22; DB 6; Length 281; 100.0%; Pred. No. 2e-14; ive 0; Mismatches 0; Indels
                                                                                          DB 6; Length 270, 2e-14;
                                                                                                                                         0; Indels
                                                                                        Query Match 61.1%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 2e-Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 59
SOCIAME: Patentin Ver. 3.2
SEQ ID NO 7
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 QQEKNEQELLELDKWASLWNWF 36
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PRIOR APPLICATION NUMBER: 60/468,835
PRIOR FILING DATE: 2003-05-06
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                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10841956A
Publication No. US20050281829A1
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: TAN HEHIR, CRISTINA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TAN HEHIR, CRISTINA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEZO, ADÁM R.
PETERS, ROBERT T.
STATTEL, JAMES M.
PALOMBELLA, VITO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PETERS, ROBERT T.
STATTEL, JAMES M.
PALOMBELLA, VITO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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EQ ID NO 6
LENGTH: 282
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Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 59
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APPLICANT:
APPLICANT:
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; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-6

Query Match

Best Local Similarity 100.0%; Pred. No. 2e-14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEGELLELDKWASLWNWF 36

Db 261 QOEKNEGELLELDKWASLWNWF 282

Search completed: March 6, 2006, 16:33:26
Job time: 11.3333 sece
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